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<110> Michael Hensel
 David William Holden
 Jacqueline Elizabeth Shea

<120> Attenuated Salmonella SPI2 Mutants as Antigen Carriers

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<151> 2001-03-02

<150> PCT/EP99/06514

<151> 1999-09-03

<150> EP 98116827.1

<151> 1998-09-04

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<170> PatentIn Ver. 2.1

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Met Met Ile Lys Lys Lys Ala Ala Phe Ser Glu Tyr Arg Asp Leu Glu
 1 5 10 15
caa agt tac atg cag cta aat cac tgt ctt aaa aaa ttt cac caa atc 96
Gln Ser Tyr Met Gln Leu Asn His Cys Leu Lys Lys Phe His Gln Ile
 20 25 30
cgg gct aag gtg agt caa cag ctt gct gaa agg gca gag agc ccc aaa 144
Arg Ala Lys Val Ser Gln Gln Leu Ala Glu Arg Ala Glu Ser Pro Lys
 35 40 45
aat agc aga gag aca gag agt att ctt cat aac cta ttt cca caa ggc 192
Asn Ser Arg Glu Thr Glu Ser Ile Leu His Asn Leu Phe Pro Gln Gly
 50 55 60
gtt gcc ggg gtt aac cag gag gcc gag aag gat tta aag aaa ata gta 240
Val Ala Gly Val Asn Gln Glu Ala Glu Lys Asp Leu Lys Lys Ile Val
 65 70 75 80
agt ttg ttt aaa caa ctt gaa gta cga ctg aaa caa ctt aat gct caa 288
Ser Leu Phe Lys Gln Leu Glu Val Arg Leu Lys Gln Leu Asn Ala Gln
 85 90 95
gcc ccg gtg gag ata ccg tca gga aaa aca aaa agg taa 327
Ala Pro Val Glu Ile Pro Ser Gly Lys Thr Lys Arg

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100

105

<210> 4
<211> 108
<212> PRT
<213> Salmonella

<400> 4

Met	Met	Ile	Lys	Lys	Lys	Ala	Ala	Phe	Ser	Glu	Tyr	Arg	Asp	Leu	Glu	
1				5					10					15		
Gln	Ser	Tyr	Met	Gln	Leu	Asn	His	Cys	Leu	Lys	Lys	Phe	His	Gln	Ile	
			20					25					30			
Arg	Ala	Lys	Val	Ser	Gln	Gln	Leu	Ala	Glu	Arg	Ala	Glu	Ser	Pro	Lys	
		35					40					45				
Asn	Ser	Arg	Glu	Thr	Glu	Ser	Ile	Leu	His	Asn	Leu	Phe	Pro	Gln	Gly	
	50					55					60					
Val	Ala	Gly	Val	Asn	Gln	Glu	Ala	Glu	Lys	Asp	Leu	Lys	Lys	Ile	Val	
	65				70					75					80	
Ser	Leu	Phe	Lys	Gln	Leu	Glu	Val	Arg	Leu	Lys	Gln	Leu	Asn	Ala	Gln	
				85					90					95		
Ala	Pro	Val	Glu	Ile	Pro	Ser	Gly	Lys	Thr	Lys	Arg					
			100					105								

<210> 5
<211> 591
<212> DNA
<213> Salmonella

<220>
<221> CDS
<222> (1)..(588)

<400> 5

atg	tct	tca	gga	aac	atc	tta	tgg	gga	agt	caa	aac	cct	att	gtg	ttt	48
Met	Ser	Ser	Gly	Asn	Ile	Leu	Trp	Gly	Ser	Gln	Asn	Pro	Ile	Val	Phe	
1				5				10						15		
aaa	aat	agc	ttc	ggc	gtc	agc	aac	gct	gat	acc	ggg	agc	cag	gat	gac	96
Lys	Asn	Ser	Phe	Gly	Val	Ser	Asn	Ala	Asp	Thr	Gly	Ser	Gln	Asp	Asp	
			20					25					30			
tta	tcc	cag	caa	aat	ccg	ttt	gcc	gaa	ggg	tat	ggt	gtt	ttg	ctt	att	144
Leu	Ser	Gln	Gln	Asn	Pro	Phe	Ala	Glu	Gly	Tyr	Gly	Val	Leu	Leu	Ile	
			35				40					45				
ctc	ctt	atg	gtt	att	cag	gct	atc	gca	aat	aat	aaa	ttt	att	gaa	gtc	192
Leu	Leu	Met	Val	Ile	Gln	Ala	Ile	Ala	Asn	Asn	Lys	Phe	Ile	Glu	Val	
		50				55					60					

cag aag aac gct gaa cgt gcc aga aat acc cag gaa aag tca aat gag 240
 Gln Lys Asn Ala Glu Arg Ala Arg Asn Thr Gln Glu Lys Ser Asn Glu
 65 70 75 80

atg gat gag gtg att gct aaa gca gcc aaa ggg gat gct aaa acc aaa 288
 Met Asp Glu Val Ile Ala Lys Ala Ala Lys Gly Asp Ala Lys Thr Lys
 85 90 95

gag gag gtg cct gag gat gta att aaa tac atg cgt gat aat ggt att 336
 Glu Glu Val Pro Glu Asp Val Ile Lys Tyr Met Arg Asp Asn Gly Ile
 100 105 110

ctc atc gat ggt atg acc att gat gat tat atg gct aaa tat ggc gat 384
 Leu Ile Asp Gly Met Thr Ile Asp Asp Tyr Met Ala Lys Tyr Gly Asp
 115 120 125

cat ggg aag ctg gat aaa ggt ggc cta cag gcg atc aaa gcg gct ttg 432
 His Gly Lys Leu Asp Lys Gly Gly Leu Gln Ala Ile Lys Ala Ala Leu
 130 135 140

gat aat gac gcc aac cgg aat acc gat ctt atg agt cag ggg cag ata 480
 Asp Asn Asp Ala Asn Arg Asn Thr Asp Leu Met Ser Gln Gly Gln Ile
 145 150 155 160

aca att caa aaa atg tct cag gag ctt aac gct gtc ctt acc caa ctg 528
 Thr Ile Gln Lys Met Ser Gln Glu Leu Asn Ala Val Leu Thr Gln Leu
 165 170 175

aca ggg ctt atc agt aag tgg ggg gaa att tcc agt atg ata gcg cag 576
 Thr Gly Leu Ile Ser Lys Trp Gly Glu Ile Ser Ser Met Ile Ala Gln
 180 185 190

aaa acg tac tca tga 591
 Lys Thr Tyr Ser
 195

<210> 6
 <211> 196
 <212> PRT
 <213> Salmonella

<400> 6
 Met Ser Ser Gly Asn Ile Leu Trp Gly Ser Gln Asn Pro Ile Val Phe
 1 5 10 15
 Lys Asn Ser Phe Gly Val Ser Asn Ala Asp Thr Gly Ser Gln Asp Asp
 20 25 30
 Leu Ser Gln Gln Asn Pro Phe Ala Glu Gly Tyr Gly Val Leu Leu Ile
 35 40 45
 Leu Leu Met Val Ile Gln Ala Ile Ala Asn Asn Lys Phe Ile Glu Val
 50 55 60
 Gln Lys Asn Ala Glu Arg Ala Arg Asn Thr Gln Glu Lys Ser Asn Glu

65					70						75					80
Met	Asp	Glu	Val	Ile	Ala	Lys	Ala	Ala	Lys	Gly	Asp	Ala	Lys	Thr	Lys	
				85					90					95		
Glu	Glu	Val	Pro	Glu	Asp	Val	Ile	Lys	Tyr	Met	Arg	Asp	Asn	Gly	Ile	
			100					105					110			
Leu	Ile	Asp	Gly	Met	Thr	Ile	Asp	Asp	Tyr	Met	Ala	Lys	Tyr	Gly	Asp	
		115					120					125				
His	Gly	Lys	Leu	Asp	Lys	Gly	Gly	Leu	Gln	Ala	Ile	Lys	Ala	Ala	Leu	
	130					135					140					
Asp	Asn	Asp	Ala	Asn	Arg	Asn	Thr	Asp	Leu	Met	Ser	Gln	Gly	Gln	Ile	
145					150					155					160	
Thr	Ile	Gln	Lys	Met	Ser	Gln	Glu	Leu	Asn	Ala	Val	Leu	Thr	Gln	Leu	
				165					170					175		
Thr	Gly	Leu	Ile	Ser	Lys	Trp	Gly	Glu	Ile	Ser	Ser	Met	Ile	Ala	Gln	
			180					185					190			
Lys	Thr	Tyr	Ser													
			195													

<210> 7
 <211> 1455
 <212> DNA
 <213> Salmonella

<220>
 <221> CDS
 <222> (1)..(1452)

<400> 7																	
atg	aat	cga	att	cac	agt	aat	agc	gac	agc	gcc	gca	gga	gta	acc	gcc		48
Met	Asn	Arg	Ile	His	Ser	Asn	Ser	Asp	Ser	Ala	Ala	Gly	Val	Thr	Ala		
	1			5					10					15			
tta	aca	cat	cat	cac	tta	agc	aat	gtc	agt	tgc	ggt	tcc	tcg	ggg	tcg		96
Leu	Thr	His	His	His	Leu	Ser	Asn	Val	Ser	Cys	Val	Ser	Ser	Gly	Ser		
			20					25					30				
ctg	gga	aag	cgc	cag	cat	cgt	gtg	aat	tct	act	ttt	ggc	gat	ggc	aac		144
Leu	Gly	Lys	Arg	Gln	His	Arg	Val	Asn	Ser	Thr	Phe	Gly	Asp	Gly	Asn		
		35					40					45					
gcc	gcg	tgt	ctg	cta	tcc	ggg	aaa	att	agt	ctt	cag	gag	gca	agc	aat		192
Ala	Ala	Cys	Leu	Leu	Ser	Gly	Lys	Ile	Ser	Leu	Gln	Glu	Ala	Ser	Asn		
	50					55					60						
gcg	ttg	aag	caa	ctg	ctt	gat	gcc	gta	ccc	gga	aat	cat	aag	cgt	cca		240
Ala	Leu	Lys	Gln	Leu	Leu	Asp	Ala	Val	Pro	Gly	Asn	His	Lys	Arg	Pro		
	65				70					75					80		

tca ttg cct gac ttt ttg cag acc aat ccc gcg gtt tta tca atg atg	288
Ser Leu Pro Asp Phe Leu Gln Thr Asn Pro Ala Val Leu Ser Met Met	
85 90 95	
atg acg tca tta ata ctc aac gtc ttt ggt aat aac gct caa tcg tta	336
Met Thr Ser Leu Ile Leu Asn Val Phe Gly Asn Asn Ala Gln Ser Leu	
100 105 110	
tgc caa cag ctt gag cgg gca act gag gtg caa aat gca tta cgt aat	384
Cys Gln Gln Leu Glu Arg Ala Thr Glu Val Gln Asn Ala Leu Arg Asn	
115 120 125	
aag cag gta aag gag tat cag gag cag atc cag aaa gcg ata gag cag	432
Lys Gln Val Lys Glu Tyr Gln Glu Gln Ile Gln Lys Ala Ile Glu Gln	
130 135 140	
gag gat aaa gcg cgt aaa gcg ggt att ttt ggc gct att ttt gac tgg	480
Glu Asp Lys Ala Arg Lys Ala Gly Ile Phe Gly Ala Ile Phe Asp Trp	
145 150 155 160	
att acc ggc ata ttt gaa acc gtg att ggc gcc tta aaa gtt gtg gaa	528
Ile Thr Gly Ile Phe Glu Thr Val Ile Gly Ala Leu Lys Val Val Glu	
165 170 175	
ggt ttt ctg tcc gga aat ccc gca gaa atg gct agc ggc gta gct tat	576
Gly Phe Leu Ser Gly Asn Pro Ala Glu Met Ala Ser Gly Val Ala Tyr	
180 185 190	
atg gcc gca ggt tgt gca gga atg gtt aaa gcc gga gcc gaa acg gca	624
Met Ala Ala Gly Cys Ala Gly Met Val Lys Ala Gly Ala Glu Thr Ala	
195 200 205	
atg atg tgc ggt gct gac cac gat acc tgt cag gca att att gac gtg	672
Met Met Cys Gly Ala Asp His Asp Thr Cys Gln Ala Ile Ile Asp Val	
210 215 220	
aca agt aag att caa ttt ggt tgt gaa gcc gtc gcg ctg gca ctg gat	720
Thr Ser Lys Ile Gln Phe Gly Cys Glu Ala Val Ala Leu Ala Leu Asp	
225 230 235 240	
gtt ttc cag att ggc cgt gct ttt atg gcg acg aga ggt tta tct ggc	768
Val Phe Gln Ile Gly Arg Ala Phe Met Ala Thr Arg Gly Leu Ser Gly	
245 250 255	
gca gct gca aaa gtg ctt gac tcc ggt ttt ggc gag gaa gtg gtt gag	816
Ala Ala Ala Lys Val Leu Asp Ser Gly Phe Gly Glu Glu Val Val Glu	
260 265 270	
cgt atg gta ggt gca ggg gaa gca gaa ata gag gag ttg gct gaa aag	864
Arg Met Val Gly Ala Gly Glu Ala Glu Ile Glu Glu Leu Ala Glu Lys	
275 280 285	
ttt ggc gaa gaa gtg agc gaa agt ttt tcc aaa caa ttt gag ccg ctt	912
Phe Gly Glu Glu Val Ser Glu Ser Phe Ser Lys Gln Phe Glu Pro Leu	
290 295 300	

gaa cgt gaa atg gct atg gcg aat gag atg gca gag gag gct gcc gag 960
Glu Arg Glu Met Ala Met Ala Asn Glu Met Ala Glu Glu Ala Ala Glu
305 310 315 320

ttt tct cgt aac gta gaa aat aat atg acg cga agc gcg gga aaa agc 1008
Phe Ser Arg Asn Val Glu Asn Asn Met Thr Arg Ser Ala Gly Lys Ser
325 330 335

ttt acg aaa gag ggg gtg aaa gcc atg gca aaa gaa gcg gca aaa gaa 1056
Phe Thr Lys Glu Gly Val Lys Ala Met Ala Lys Glu Ala Ala Lys Glu
340 345 350

gcc ctg gaa aaa tgt gtg caa gaa ggt gga aag ttc ctg tta aaa aaa 1104
Ala Leu Glu Lys Cys Val Gln Glu Gly Gly Lys Phe Leu Leu Lys Lys
355 360 365

ttc cgt aat aaa gtt ctc ttc aat atg ttc aaa aaa atc ctg tat gcc 1152
Phe Arg Asn Lys Val Leu Phe Asn Met Phe Lys Lys Ile Leu Tyr Ala
370 375 380

tta ctg agg gat tgt tca ttt aaa ggc tta cag gct atc aga tgt gca 1200
Leu Leu Arg Asp Cys Ser Phe Lys Gly Leu Gln Ala Ile Arg Cys Ala
385 390 395 400

acc gag ggc gcc agt cag atg aat act ggc atg gtt aac aca gaa aaa 1248
Thr Glu Gly Ala Ser Gln Met Asn Thr Gly Met Val Asn Thr Glu Lys
405 410 415

gcg aag atc gaa aag aaa ata gag caa tta ata act cag caa cgg ttt 1296
Ala Lys Ile Glu Lys Lys Ile Glu Gln Leu Ile Thr Gln Gln Arg Phe
420 425 430

ctg gat ttc ata atg caa caa aca gaa aac cag aaa aag ata gaa caa 1344
Leu Asp Phe Ile Met Gln Gln Thr Glu Asn Gln Lys Lys Ile Glu Gln
435 440 445

aaa cgc tta gag gag ctt tat aag ggg acg ggt gcc gcg ctt aga gat 1392
Lys Arg Leu Glu Glu Leu Tyr Lys Gly Thr Gly Ala Ala Leu Arg Asp
450 455 460

gta tta gat acc att gat cac tat agt agc gtt cag gcg aga ata gct 1440
Val Leu Asp Thr Ile Asp His Tyr Ser Ser Val Gln Ala Arg Ile Ala
465 470 475 480

ggc tat cgc gct taa 1455
Gly Tyr Arg Ala

<210> 8
<211> 484
<212> PRT
<213> Salmonella

<400> 8
Met Asn Arg Ile His Ser Asn Ser Asp Ser Ala Ala Gly Val Thr Ala
1 5 10 15

Leu Thr His His His Leu Ser Asn Val Ser Cys Val Ser Ser Gly Ser
20 25 30

Leu Gly Lys Arg Gln His Arg Val Asn Ser Thr Phe Gly Asp Gly Asn
35 40 45

Ala Ala Cys Leu Leu Ser Gly Lys Ile Ser Leu Gln Glu Ala Ser Asn
50 55 60

Ala Leu Lys Gln Leu Leu Asp Ala Val Pro Gly Asn His Lys Arg Pro
65 70 75 80

Ser Leu Pro Asp Phe Leu Gln Thr Asn Pro Ala Val Leu Ser Met Met
85 90 95

Met Thr Ser Leu Ile Leu Asn Val Phe Gly Asn Asn Ala Gln Ser Leu
100 105 110

Cys Gln Gln Leu Glu Arg Ala Thr Glu Val Gln Asn Ala Leu Arg Asn
115 120 125

Lys Gln Val Lys Glu Tyr Gln Glu Gln Ile Gln Lys Ala Ile Glu Gln
130 135 140

Glu Asp Lys Ala Arg Lys Ala Gly Ile Phe Gly Ala Ile Phe Asp Trp
145 150 155 160

Ile Thr Gly Ile Phe Glu Thr Val Ile Gly Ala Leu Lys Val Val Glu
165 170 175

Gly Phe Leu Ser Gly Asn Pro Ala Glu Met Ala Ser Gly Val Ala Tyr
180 185 190

Met Ala Ala Gly Cys Ala Gly Met Val Lys Ala Gly Ala Glu Thr Ala
195 200 205

Met Met Cys Gly Ala Asp His Asp Thr Cys Gln Ala Ile Ile Asp Val
210 215 220

Thr Ser Lys Ile Gln Phe Gly Cys Glu Ala Val Ala Leu Ala Leu Asp
225 230 235 240

Val Phe Gln Ile Gly Arg Ala Phe Met Ala Thr Arg Gly Leu Ser Gly
245 250 255

Ala Ala Ala Lys Val Leu Asp Ser Gly Phe Gly Glu Glu Val Val Glu
260 265 270

Arg Met Val Gly Ala Gly Glu Ala Glu Ile Glu Glu Leu Ala Glu Lys
275 280 285

Phe Gly Glu Glu Val Ser Glu Ser Phe Ser Lys Gln Phe Glu Pro Leu
290 295 300

Glu Arg Glu Met Ala Met Ala Asn Glu Met Ala Glu Glu Ala Ala Glu
305 310 315 320

Phe Ser Arg Asn Val Glu Asn Asn Met Thr Arg Ser Ala Gly Lys Ser
 325 330 335
 Phe Thr Lys Glu Gly Val Lys Ala Met Ala Lys Glu Ala Ala Lys Glu
 340 345 350
 Ala Leu Glu Lys Cys Val Gln Glu Gly Gly Lys Phe Leu Leu Lys Lys
 355 360 365
 Phe Arg Asn Lys Val Leu Phe Asn Met Phe Lys Lys Ile Leu Tyr Ala
 370 375 380
 Leu Leu Arg Asp Cys Ser Phe Lys Gly Leu Gln Ala Ile Arg Cys Ala
 385 390 395 400
 Thr Glu Gly Ala Ser Gln Met Asn Thr Gly Met Val Asn Thr Glu Lys
 405 410 415
 Ala Lys Ile Glu Lys Lys Ile Glu Gln Leu Ile Thr Gln Gln Arg Phe
 420 425 430
 Leu Asp Phe Ile Met Gln Gln Thr Glu Asn Gln Lys Lys Ile Glu Gln
 435 440 445
 Lys Arg Leu Glu Glu Leu Tyr Lys Gly Thr Gly Ala Ala Leu Arg Asp
 450 455 460
 Val Leu Asp Thr Ile Asp His Tyr Ser Ser Val Gln Ala Arg Ile Ala
 465 470 475 480
 Gly Tyr Arg Ala

<210> 9
 <211> 504
 <212> DNA
 <213> Salmonella

<220>
 <221> CDS
 <222> (1)..(501)

<400> 9
 atg ggt act gaa tca atg ctt ctg tta ttt gat gat atc tgg atg aag 48
 Met Gly Thr Glu Ser Met Leu Leu Leu Phe Asp Asp Ile Trp Met Lys
 1 5 10 15
 cta atg gag ctt gcc aaa aag ctg cgc gat atc atg cgc agc tat aac 96
 Leu Met Glu Leu Ala Lys Lys Leu Arg Asp Ile Met Arg Ser Tyr Asn
 20 25 30
 gta gaa aaa caa cgg ctg gcc tgg gaa ctg caa gtc aat gtt tta cag 144
 Val Glu Lys Gln Arg Leu Ala Trp Glu Leu Gln Val Asn Val Leu Gln
 35 40 45

acg caa atg aaa aca att gat gaa gcg ttt aga gca tca atg att act 192
Thr Gln Met Lys Thr Ile Asp Glu Ala Phe Arg Ala Ser Met Ile Thr
50 55 60

gcg ggt ggc gca atg ttg tcg ggt gta ctg acg ata gga tta ggg gcc 240
Ala Gly Gly Ala Met Leu Ser Gly Val Leu Thr Ile Gly Leu Gly Ala
65 70 75 80

gta ggc ggg gaa acc ggt ctt ata gcg ggt caa gcc gta ggc cac aca 288
Val Gly Gly Glu Thr Gly Leu Ile Ala Gly Gln Ala Val Gly His Thr
85 90 95

gct ggg ggc gtc atg ggc ctg ggg gct ggt gta gcg caa cgt caa agt 336
Ala Gly Gly Val Met Gly Leu Gly Ala Gly Val Ala Gln Arg Gln Ser
100 105 110

gat caa gat aaa gcg att gcc gac ctg caa caa aat ggg gcc caa tct 384
Asp Gln Asp Lys Ala Ile Ala Asp Leu Gln Gln Asn Gly Ala Gln Ser
115 120 125

tat aat aaa tcc ctg acg gaa att atg gag aaa gca act gaa att atg 432
Tyr Asn Lys Ser Leu Thr Glu Ile Met Glu Lys Ala Thr Glu Ile Met
130 135 140

cag caa atc atc ggc gtg ggg tcg tca ctg gtc acg gtt ctt gct gaa 480
Gln Gln Ile Ile Gly Val Gly Ser Ser Leu Val Thr Val Leu Ala Glu
145 150 155 160

ata ctc cgg gca tta acg agg taa 504
Ile Leu Arg Ala Leu Thr Arg
165

<210> 10
<211> 167
<212> PRT
<213> Salmonella

<400> 10
Met Gly Thr Glu Ser Met Leu Leu Leu Phe Asp Asp Ile Trp Met Lys
1 5 10 15

Leu Met Glu Leu Ala Lys Lys Leu Arg Asp Ile Met Arg Ser Tyr Asn
20 25 30

Val Glu Lys Gln Arg Leu Ala Trp Glu Leu Gln Val Asn Val Leu Gln
35 40 45

Thr Gln Met Lys Thr Ile Asp Glu Ala Phe Arg Ala Ser Met Ile Thr
50 55 60

Ala Gly Gly Ala Met Leu Ser Gly Val Leu Thr Ile Gly Leu Gly Ala
65 70 75 80

Val Gly Gly Glu Thr Gly Leu Ile Ala Gly Gln Ala Val Gly His Thr
85 90 95

Ala Gly Gly Val Met Gly Leu Gly Ala Gly Val Ala Gln Arg Gln Ser
100 105 110

Asp Gln Asp Lys Ala Ile Ala Asp Leu Gln Gln Asn Gly Ala Gln Ser
115 120 125

Tyr Asn Lys Ser Leu Thr Glu Ile Met Glu Lys Ala Thr Glu Ile Met
130 135 140

Gln Gln Ile Ile Gly Val Gly Ser Ser Leu Val Thr Val Leu Ala Glu
145 150 155 160

Ile Leu Arg Ala Leu Thr Arg
165

<210> 11
<211> 195
<212> PRT
<213> Salmonella

<400> 11
Met Glu Ala Ser Asn Val Ala Leu Val Leu Pro Ala Pro Ser Leu Leu
1 5 10 15

Thr Pro Ser Ser Thr Pro Ser Pro Ser Gly Glu Gly Met Gly Thr Glu
20 25 30

Ser Met Leu Leu Leu Phe Asp Asp Ile Trp Met Lys Leu Met Glu Leu
35 40 45

Ala Lys Lys Leu Arg Asp Ile Met Arg Ser Tyr Asn Val Glu Lys Gln
50 55 60

Arg Leu Ala Trp Glu Leu Gln Val Asn Val Leu Gln Thr Gln Met Lys
65 70 75 80

Thr Ile Asp Glu Ala Phe Arg Ala Ser Met Ile Thr Ala Gly Gly Ala
85 90 95

Met Leu Ser Gly Val Leu Thr Ile Gly Leu Gly Ala Val Gly Gly Glu
100 105 110

Thr Gly Leu Ile Ala Gly Gln Ala Val Gly His Thr Ala Gly Gly Val
115 120 125

Met Gly Leu Gly Ala Gly Val Ala Gln Arg Gln Ser Asp Gln Asp Lys
130 135 140

Ala Ile Ala Asp Leu Gln Gln Asn Gly Ala Gln Ser Tyr Asn Lys Ser
145 150 155 160

Leu Thr Glu Ile Met Glu Lys Ala Thr Glu Ile Met Gln Gln Ile Ile
165 170 175

Gly Val Gly Ser Ser Leu Val Thr Val Leu Ala Glu Ile Leu Arg Ala

180

185

190

Leu Thr Arg
195

<210> 12
<211> 417
<212> DNA
<213> Salmonella

<220>
<221> CDS
<222> (1)..(414)

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<400> 12
atg gtg caa gaa ata gag caa tgg tta cgt cgg cat cag gtg ttt act 48
Met Val Gln Glu Ile Glu Gln Trp Leu Arg Arg His Gln Val Phe Thr
  1                5                10                15

gag cct gca tat tta ggg gag acc gcc ata tta ctt ggg cag cag ttt 96
Glu Pro Ala Tyr Leu Gly Glu Thr Ala Ile Leu Leu Gly Gln Gln Phe
                20                25                30

ata tta tcg cct tac ctg gtg atc tat cgt att gag gca aaa gaa atg 144
Ile Leu Ser Pro Tyr Leu Val Ile Tyr Arg Ile Glu Ala Lys Glu Met
                35                40                45

att att tgt gag ttc agg cgc ctg acg ccc ggg caa cct cga cca cag 192
Ile Ile Cys Glu Phe Arg Arg Leu Thr Pro Gly Gln Pro Arg Pro Gln
                50                55                60

caa ttg ttt cac tta ctg gga ctt tta cgc ggg ata ttt gtg cat cac 240
Gln Leu Phe His Leu Leu Gly Leu Leu Arg Gly Ile Phe Val His His
  65                70                75                80

ccg cag tta aca tgt tta aag atg ttg ata atc acc gac gtt ctg gat 288
Pro Gln Leu Thr Cys Leu Lys Met Leu Ile Ile Thr Asp Val Leu Asp
                85                90                95

gaa aaa aaa gcc atg cta cgc agg aaa tta ttg cgc atc ctg aca gta 336
Glu Lys Lys Ala Met Leu Arg Arg Lys Leu Leu Arg Ile Leu Thr Val
                100                105                110

atg gga gcg acc ttt aca cag ctt gat ggc gat aac tgg aca gtt tta 384
Met Gly Ala Thr Phe Thr Gln Leu Asp Gly Asp Asn Trp Thr Val Leu
                115                120                125

tcc gcc gag cat ctt atc cag cga cgt ttt taa 417
Ser Ala Glu His Leu Ile Gln Arg Arg Phe
  130                135

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<210> 13
<211> 138
<212> PRT

<213> Salmonella

<400> 13

Met Val Gln Glu Ile Glu Gln Trp Leu Arg Arg His Gln Val Phe Thr
1 5 10 15
Glu Pro Ala Tyr Leu Gly Glu Thr Ala Ile Leu Leu Gly Gln Gln Phe
20 25 30
Ile Leu Ser Pro Tyr Leu Val Ile Tyr Arg Ile Glu Ala Lys Glu Met
35 40 45
Ile Ile Cys Glu Phe Arg Arg Leu Thr Pro Gly Gln Pro Arg Pro Gln
50 55 60
Gln Leu Phe His Leu Leu Gly Leu Leu Arg Gly Ile Phe Val His His
65 70 75 80
Pro Gln Leu Thr Cys Leu Lys Met Leu Ile Ile Thr Asp Val Leu Asp
85 90 95
Glu Lys Lys Ala Met Leu Arg Arg Lys Leu Leu Arg Ile Leu Thr Val
100 105 110
Met Gly Ala Thr Phe Thr Gln Leu Asp Gly Asp Asn Trp Thr Val Leu
115 120 125
Ser Ala Glu His Leu Ile Gln Arg Arg Phe
130 135

<210> 14

<211> 789

<212> DNA

<213> Salmonella

<220>

<221> CDS

<222> (1)..(786)

<400> 14

atg aaa att cat att ccg tca gcg gca agt aat ata gtc gat ggt aat 48
Met Lys Ile His Ile Pro Ser Ala Ala Ser Asn Ile Val Asp Gly Asn
1 5 10 15
agt cct cct tcc gat ata caa gcg aag gag gta tcg ttt cct ccc cct 96
Ser Pro Pro Ser Asp Ile Gln Ala Lys Glu Val Ser Phe Pro Pro Pro
20 25 30
gaa att cca gcg cct ggc acc ccc gca gcc cct gtg ctg ctt acg cct 144
Glu Ile Pro Ala Pro Gly Thr Pro Ala Ala Pro Val Leu Leu Thr Pro
35 40 45
gaa caa ata agg cag cag agg gat tat gcg ata cat ttt atg caa tac 192
Glu Gln Ile Arg Gln Gln Arg Asp Tyr Ala Ile His Phe Met Gln Tyr
50 55 60

act att cgt gcg ctg ggt gcg aca gtc gtg ttt ggg tta tcg gtt gct 240
Thr Ile Arg Ala Leu Gly Ala Thr Val Val Phe Gly Leu Ser Val Ala
65 70 75 80

gca gcg gta att tct ggc ggg gca gga tta ccc att gct att ctt gcg 288
Ala Ala Val Ile Ser Gly Gly Ala Gly Leu Pro Ile Ala Ile Leu Ala
85 90 95

ggg gcg gcg ctc gtg att gct att ggg gat gct tgc tgt gcg tat cat 336
Gly Ala Ala Leu Val Ile Ala Ile Gly Asp Ala Cys Cys Ala Tyr His
100 105 110

aat tat caa tcg ata tgt cag caa aag gag cca tta caa acc gcc agt 384
Asn Tyr Gln Ser Ile Cys Gln Gln Lys Glu Pro Leu Gln Thr Ala Ser
115 120 125

gat agc gtt gct ctt gtg gtc agt gcg ctg gcc tta aaa tgt ggg gca 432
Asp Ser Val Ala Leu Val Val Ser Ala Leu Ala Leu Lys Cys Gly Ala
130 135 140

agt ctt aac tgc gct aac acc ctt gct aat tgt ctt tct tta tta ata 480
Ser Leu Asn Cys Ala Asn Thr Leu Ala Asn Cys Leu Ser Leu Leu Ile
145 150 155 160

cgt tca gga atc gct att tct atg ttg gtt tta ccc cta cag ttt cca 528
Arg Ser Gly Ile Ala Ile Ser Met Leu Val Leu Pro Leu Gln Phe Pro
165 170 175

ctg ccc gcg gct gaa aat att gcg gcc tct ttg gac atg ggg agt gta 576
Leu Pro Ala Ala Glu Asn Ile Ala Ala Ser Leu Asp Met Gly Ser Val
180 185 190

att acc tcc gtt agc ctg acg gcg ata ggt gcg gta ctg gat tat tgc 624
Ile Thr Ser Val Ser Leu Thr Ala Ile Gly Ala Val Leu Asp Tyr Cys
195 200 205

ctt gcc cgc ccc tct ggc gac gat cag gaa aat tct gtt gat gaa ctt 672
Leu Ala Arg Pro Ser Gly Asp Asp Gln Glu Asn Ser Val Asp Glu Leu
210 215 220

cat gcc gat ccc agt gtg tta ttg gcg gaa caa atg gca gcg ctc tgt 720
His Ala Asp Pro Ser Val Leu Leu Ala Glu Gln Met Ala Ala Leu Cys
225 230 235 240

caa tct gct act aca cct gca cct gca tta atg gac agt tct gat cat 768
Gln Ser Ala Thr Thr Pro Ala Pro Ala Leu Met Asp Ser Ser Asp His
245 250 255

aca tct cgg gga gaa cca tga 789
Thr Ser Arg Gly Glu Pro
260

<210> 15
<211> 262
<212> PRT

<213> Salmonella

<400> 15

Met Lys Ile His Ile Pro Ser Ala Ala Ser Asn Ile Val Asp Gly Asn
1 5 10 15
Ser Pro Pro Ser Asp Ile Gln Ala Lys Glu Val Ser Phe Pro Pro Pro
20 25 30
Glu Ile Pro Ala Pro Gly Thr Pro Ala Ala Pro Val Leu Leu Thr Pro
35 40 45
Glu Gln Ile Arg Gln Gln Arg Asp Tyr Ala Ile His Phe Met Gln Tyr
50 55 60
Thr Ile Arg Ala Leu Gly Ala Thr Val Val Phe Gly Leu Ser Val Ala
65 70 75 80
Ala Ala Val Ile Ser Gly Gly Ala Gly Leu Pro Ile Ala Ile Leu Ala
85 90 95
Gly Ala Ala Leu Val Ile Ala Ile Gly Asp Ala Cys Cys Ala Tyr His
100 105 110
Asn Tyr Gln Ser Ile Cys Gln Gln Lys Glu Pro Leu Gln Thr Ala Ser
115 120 125
Asp Ser Val Ala Leu Val Val Ser Ala Leu Ala Leu Lys Cys Gly Ala
130 135 140
Ser Leu Asn Cys Ala Asn Thr Leu Ala Asn Cys Leu Ser Leu Leu Ile
145 150 155 160
Arg Ser Gly Ile Ala Ile Ser Met Leu Val Leu Pro Leu Gln Phe Pro
165 170 175
Leu Pro Ala Ala Glu Asn Ile Ala Ala Ser Leu Asp Met Gly Ser Val
180 185 190
Ile Thr Ser Val Ser Leu Thr Ala Ile Gly Ala Val Leu Asp Tyr Cys
195 200 205
Leu Ala Arg Pro Ser Gly Asp Asp Gln Glu Asn Ser Val Asp Glu Leu
210 215 220
His Ala Asp Pro Ser Val Leu Leu Ala Glu Gln Met Ala Ala Leu Cys
225 230 235 240
Gln Ser Ala Thr Thr Pro Ala Pro Ala Leu Met Asp Ser Ser Asp His
245 250 255
Thr Ser Arg Gly Glu Pro
260

<210> 16

<211> 690
<212> DNA
<213> Salmonella

<220>
<221> CDS
<222> (1)..(687)

<400> 16

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atg aaa cct gtt agc cca aat gct cag gta gga ggg caa cgt cct gtt 48
Met Lys Pro Val Ser Pro Asn Ala Gln Val Gly Gly Gln Arg Pro Val
  1                    5                    10                    15

aac gcg cct gag gaa tca cct cca tgt cct tca ttg cca cat ccg gaa 96
Asn Ala Pro Glu Glu Ser Pro Pro Cys Pro Ser Leu Pro His Pro Glu
                20                    25                    30

acc aat atg gag agt ggt aga ata gga cct caa caa gga aaa gag cgg 144
Thr Asn Met Glu Ser Gly Arg Ile Gly Pro Gln Gln Gly Lys Glu Arg
                35                    40                    45

gta ttg gcc gga ctt gcg aaa cga gtg ata gag tgt ttt cca aaa gaa 192
Val Leu Ala Gly Leu Ala Lys Arg Val Ile Glu Cys Phe Pro Lys Glu
  50                    55                    60

att ttt agt tgg caa acg gtt att ttg ggc gga cag att tta tgc tgt 240
Ile Phe Ser Trp Gln Thr Val Ile Leu Gly Gly Gln Ile Leu Cys Cys
  65                    70                    75                    80

tcc gct gga ata gca tta aca gtg cta agt ggt gga ggc gcg ccg ctc 288
Ser Ala Gly Ile Ala Leu Thr Val Leu Ser Gly Gly Gly Ala Pro Leu
                85                    90                    95

gta gcc ctg gca ggg att ggc ctt gct att gcc atc gcg gat gtc gcc 336
Val Ala Leu Ala Gly Ile Gly Leu Ala Ile Ala Ile Ala Asp Val Ala
                100                    105                    110

tgt ctt atc tac cat cat aaa cat cat ttg cct atg gct cac gac agt 384
Cys Leu Ile Tyr His His Lys His His Leu Pro Met Ala His Asp Ser
                115                    120                    125

ata ggc aat gcc gtt ttt tat att gct aat tgt ttc gcc aat caa cgc 432
Ile Gly Asn Ala Val Phe Tyr Ile Ala Asn Cys Phe Ala Asn Gln Arg
                130                    135                    140

aaa agt atg gcg att gct aaa gcc gtc tcc ctg ggc ggt aga tta gcc 480
Lys Ser Met Ala Ile Ala Lys Ala Val Ser Leu Gly Gly Arg Leu Ala
  145                    150                    155                    160

tta acc gcg acg gta atg act cat tca tac tgg agt ggt agt ttg gga 528
Leu Thr Ala Thr Val Met Thr His Ser Tyr Trp Ser Gly Ser Leu Gly
                165                    170                    175

cta cag cct cat tta tta gag cgt ctt aat gat att acc tat gga cta 576
Leu Gln Pro His Leu Leu Glu Arg Leu Asn Asp Ile Thr Tyr Gly Leu
                180                    185                    190
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atg agt ttt act cgc ttc ggt atg gat ggg atg gca atg acc ggt atg 624
Met Ser Phe Thr Arg Phe Gly Met Asp Gly Met Ala Met Thr Gly Met
195 200 205

cag gtc agc agc cca tta tat cgt ttg ctg gct cag gta acg cca gaa 672
Gln Val Ser Ser Pro Leu Tyr Arg Leu Leu Ala Gln Val Thr Pro Glu
210 215 220

caa cgt gcg ccg gag taa 690
Gln Arg Ala Pro Glu
225

<210> 17
<211> 229
<212> PRT
<213> Salmonella

<400> 17
Met Lys Pro Val Ser Pro Asn Ala Gln Val Gly Gly Gln Arg Pro Val
1 5 10 15

Asn Ala Pro Glu Glu Ser Pro Pro Cys Pro Ser Leu Pro His Pro Glu
20 25 30

Thr Asn Met Glu Ser Gly Arg Ile Gly Pro Gln Gln Gly Lys Glu Arg
35 40 45

Val Leu Ala Gly Leu Ala Lys Arg Val Ile Glu Cys Phe Pro Lys Glu
50 55 60

Ile Phe Ser Trp Gln Thr Val Ile Leu Gly Gly Gln Ile Leu Cys Cys
65 70 75 80

Ser Ala Gly Ile Ala Leu Thr Val Leu Ser Gly Gly Gly Ala Pro Leu
85 90 95

Val Ala Leu Ala Gly Ile Gly Leu Ala Ile Ala Ile Ala Asp Val Ala
100 105 110

Cys Leu Ile Tyr His His Lys His His Leu Pro Met Ala His Asp Ser
115 120 125

Ile Gly Asn Ala Val Phe Tyr Ile Ala Asn Cys Phe Ala Asn Gln Arg
130 135 140

Lys Ser Met Ala Ile Ala Lys Ala Val Ser Leu Gly Gly Arg Leu Ala
145 150 155 160

Leu Thr Ala Thr Val Met Thr His Ser Tyr Trp Ser Gly Ser Leu Gly
165 170 175

Leu Gln Pro His Leu Leu Glu Arg Leu Asn Asp Ile Thr Tyr Gly Leu
180 185 190

Met Ser Phe Thr Arg Phe Gly Met Asp Gly Met Ala Met Thr Gly Met
195 200 205

Gln Val Ser Ser Pro Leu Tyr Arg Leu Leu Ala Gln Val Thr Pro Glu
210 215 220

Gln Arg Ala Pro Glu
225

<210> 18
<211> 474
<212> DNA
<213> Salmonella

<220>
<221> CDS
<222> (1)..(471)

<400> 18
atg aaa aaa gac ccg acc cta caa cag gca cat gac acg atg cgg ttt 48
Met Lys Lys Asp Pro Thr Leu Gln Gln Ala His Asp Thr Met Arg Phe
1 5 10 15
ttc cgg cgt ggc ggc tcg ctg cgt atg ttg ttg gat gac gat gtt aca 96
Phe Arg Arg Gly Gly Ser Leu Arg Met Leu Leu Asp Asp Asp Val Thr
20 25 30
cag ccg ctt aat act ctg tat cgc tat gcc acg cag ctt atg gag gta 144
Gln Pro Leu Asn Thr Leu Tyr Arg Tyr Ala Thr Gln Leu Met Glu Val
35 40 45
aaa gaa ttc gcc ggc gca gcg cga ctt ttt caa ttg ctg acg ata tat 192
Lys Glu Phe Ala Gly Ala Ala Arg Leu Phe Gln Leu Leu Thr Ile Tyr
50 55 60
gat gcc tgg tca ttt gac tac tgg ttt cgg tta ggg gaa tgc tgc cag 240
Asp Ala Trp Ser Phe Asp Tyr Trp Phe Arg Leu Gly Glu Cys Cys Gln
65 70 75 80
gct caa aaa cat tgg ggg gaa gcg ata tac gct tat gga cgc gcg gca 288
Ala Gln Lys His Trp Gly Glu Ala Ile Tyr Ala Tyr Gly Arg Ala Ala
85 90 95
caa att aag att gat gcg ccg cag gcg cca tgg gcc gca gcg gaa tgc 336
Gln Ile Lys Ile Asp Ala Pro Gln Ala Pro Trp Ala Ala Ala Glu Cys
100 105 110
tat ctc gcg tgt gat aac gtc tgt tat gca atc aaa gcg tta aag gcc 384
Tyr Leu Ala Cys Asp Asn Val Cys Tyr Ala Ile Lys Ala Leu Lys Ala
115 120 125
gtg gtg cgt att tgc ggc gag gtc agt gaa cat caa att ctc cga cag 432
Val Val Arg Ile Cys Gly Glu Val Ser Glu His Gln Ile Leu Arg Gln
130 135 140
cgt gca gaa aag atg tta cag caa ctt tct gac agg agc taa 474
Arg Ala Glu Lys Met Leu Gln Gln Leu Ser Asp Arg Ser

145

150

155

<210> 19

<211> 157

<212> PRT

<213> Salmonella

<400> 19

Met	Lys	Lys	Asp	Pro	Thr	Leu	Gln	Gln	Ala	His	Asp	Thr	Met	Arg	Phe
1				5					10					15	

Phe	Arg	Arg	Gly	Gly	Ser	Leu	Arg	Met	Leu	Leu	Asp	Asp	Asp	Val	Thr
			20					25					30		

Gln	Pro	Leu	Asn	Thr	Leu	Tyr	Arg	Tyr	Ala	Thr	Gln	Leu	Met	Glu	Val
		35					40					45			

Lys	Glu	Phe	Ala	Gly	Ala	Ala	Arg	Leu	Phe	Gln	Leu	Leu	Thr	Ile	Tyr
	50					55					60				

Asp	Ala	Trp	Ser	Phe	Asp	Tyr	Trp	Phe	Arg	Leu	Gly	Glu	Cys	Cys	Gln
65					70					75					80

Ala	Gln	Lys	His	Trp	Gly	Glu	Ala	Ile	Tyr	Ala	Tyr	Gly	Arg	Ala	Ala
				85					90					95	

Gln	Ile	Lys	Ile	Asp	Ala	Pro	Gln	Ala	Pro	Trp	Ala	Ala	Ala	Glu	Cys
			100					105					110		

Tyr	Leu	Ala	Cys	Asp	Asn	Val	Cys	Tyr	Ala	Ile	Lys	Ala	Leu	Lys	Ala
		115					120					125			

Val	Val	Arg	Ile	Cys	Gly	Glu	Val	Ser	Glu	His	Gln	Ile	Leu	Arg	Gln
	130					135					140				

Arg	Ala	Glu	Lys	Met	Leu	Gln	Gln	Leu	Ser	Asp	Arg	Ser
145					150					155		

<210> 20

<211> 435

<212> DNA

<213> Salmonella

<220>

<221> CDS

<222> (1)..(432)

<400> 20

atg	atg	atg	aaa	gaa	gat	cag	aaa	aat	aaa	ata	ccc	gaa	gac	att	ctg	48
Met	Met	Met	Lys	Glu	Asp	Gln	Lys	Asn	Lys	Ile	Pro	Glu	Asp	Ile	Leu	
1				5					10					15		

aaa	cag	cta	tta	tcc	ggt	gat	ccg	gaa	acc	ggt	tat	gcc	agt	ggt	tac	96
Lys	Gln	Leu	Leu	Ser	Val	Asp	Pro	Glu	Thr	Val	Tyr	Ala	Ser	Gly	Tyr	

	20		25		30	
gcc tca tgg cag gag ggg gat tat tgc cgc gcc gta atc gat ttt agt						144
Ala Ser Trp Gln Glu Gly Asp Tyr Ser Arg Ala Val Ile Asp Phe Ser						
	35		40		45	
tgg ctg gtg atg gcc cag cca tgg agt tgg cgt gcc cat att gca ttg						192
Trp Leu Val Met Ala Gln Pro Trp Ser Trp Arg Ala His Ile Ala Leu						
	50		55		60	
gct ggc acc tgg atg atg ctt aaa gaa tac acg acg gcc att aat ttc						240
Ala Gly Thr Trp Met Met Leu Lys Glu Tyr Thr Thr Ala Ile Asn Phe						
	65		70		75	80
tat gga cat gcc ttg atg ctg gat gcc agc cat cca gaa ccg gtt tac						288
Tyr Gly His Ala Leu Met Leu Asp Ala Ser His Pro Glu Pro Val Tyr						
	85		90		95	
caa acg ggc gtc tgt ctc aaa atg atg ggg gaa ccc ggg ttg gcg aga						336
Gln Thr Gly Val Cys Leu Lys Met Met Gly Glu Pro Gly Leu Ala Arg						
	100		105		110	
gag gct ttt caa acc gca atc aag atg agt tat gcg gat gcc tca tgg						384
Glu Ala Phe Gln Thr Ala Ile Lys Met Ser Tyr Ala Asp Ala Ser Trp						
	115		120		125	
agt gag att cgc cag aat gcg caa ata atg gtt gat act ctt att gct						432
Ser Glu Ile Arg Gln Asn Ala Gln Ile Met Val Asp Thr Leu Ile Ala						
	130		135		140	
taa						435

<210> 21
 <211> 144
 <212> PRT
 <213> Salmonella

<400> 21	
Met Met Met Lys Glu Asp Gln Lys Asn Lys Ile Pro Glu Asp Ile Leu	
1	5 10 15
Lys Gln Leu Leu Ser Val Asp Pro Glu Thr Val Tyr Ala Ser Gly Tyr	
	20 25 30
Ala Ser Trp Gln Glu Gly Asp Tyr Ser Arg Ala Val Ile Asp Phe Ser	
	35 40 45
Trp Leu Val Met Ala Gln Pro Trp Ser Trp Arg Ala His Ile Ala Leu	
	50 55 60
Ala Gly Thr Trp Met Met Leu Lys Glu Tyr Thr Thr Ala Ile Asn Phe	
	65 70 75 80
Tyr Gly His Ala Leu Met Leu Asp Ala Ser His Pro Glu Pro Val Tyr	
	85 90 95

Gln Thr Gly Val Cys Leu Lys Met Met Gly Glu Pro Gly Leu Ala Arg
 100 105 110

Glu Ala Phe Gln Thr Ala Ile Lys Met Ser Tyr Ala Asp Ala Ser Trp
 115 120 125

Ser Glu Ile Arg Gln Asn Ala Gln Ile Met Val Asp Thr Leu Ile Ala
 130 135 140

<210> 22
 <211> 1212
 <212> DNA
 <213> Salmonella

<220>
 <221> CDS
 <222> (1)..(1209)

<400> 22
 atg gca tat ctc atg gtt aat cca aag agt tcc tgg aaa ata cgt ttt 48
 Met Ala Tyr Leu Met Val Asn Pro Lys Ser Ser Trp Lys Ile Arg Phe
 1 5 10 15

tta ggt cac gtt tta caa ggc cgg gaa gta tgg ctg aat gaa ggt aac 96
 Leu Gly His Val Leu Gln Gly Arg Glu Val Trp Leu Asn Glu Gly Asn
 20 25 30

ctg tca ctg ggg gag aag gga tgc gat att tgt att ccg ctg gct ata 144
 Leu Ser Leu Gly Glu Lys Gly Cys Asp Ile Cys Ile Pro Leu Ala Ile
 35 40 45

aat gaa aaa att att ctg aga gaa cag gca gat agt tta ttt gtt gat 192
 Asn Glu Lys Ile Ile Leu Arg Glu Gln Ala Asp Ser Leu Phe Val Asp
 50 55 60

gcc ggg aaa gcc aga gtt aga gtt aat ggc cgc aga ttt aat cca aat 240
 Ala Gly Lys Ala Arg Val Arg Val Asn Gly Arg Arg Phe Asn Pro Asn
 65 70 75 80

aag ccg cta cca tcc agt ggg gtt ttg cag gtt gcg gga gtg gct atc 288
 Lys Pro Leu Pro Ser Ser Gly Val Leu Gln Val Ala Gly Val Ala Ile
 85 90 95

gcg ttt ggt aaa cag gat tgt gaa ctt gct gat tat caa ata ccc gtt 336
 Ala Phe Gly Lys Gln Asp Cys Glu Leu Ala Asp Tyr Gln Ile Pro Val
 100 105 110

tcc aga tca ggg tac tgg tgg ttg gct ggc gta ttc ttg att ttc atc 384
 Ser Arg Ser Gly Tyr Trp Trp Leu Ala Gly Val Phe Leu Ile Phe Ile
 115 120 125

ggt gga atg ggt gtc ctg tta agt att agt ggt cag cct gaa acg gta 432
 Gly Gly Met Gly Val Leu Leu Ser Ile Ser Gly Gln Pro Glu Thr Val
 130 135 140

aat gac tta cct ttg cgg gtt aag ttt tta tta gac aaa agc aat att	480
Asn Asp Leu Pro Leu Arg Val Lys Phe Leu Leu Asp Lys Ser Asn Ile	
145 150 155 160	
cat tat gtg cgg gcg caa tgg aaa gaa gat ggc agc ctg cag ttg tcc	528
His Tyr Val Arg Ala Gln Trp Lys Glu Asp Gly Ser Leu Gln Leu Ser	
165 170 175	
ggt tat tgc tcg tca agc gaa cag atg caa aag gtg aga gcg act ctc	576
Gly Tyr Cys Ser Ser Ser Glu Gln Met Gln Lys Val Arg Ala Thr Leu	
180 185 190	
gaa tca tgg ggg gtc atg tat cgg gat ggt gta atc tgt gat gac tta	624
Glu Ser Trp Gly Val Met Tyr Arg Asp Gly Val Ile Cys Asp Asp Leu	
195 200 205	
ttg gta cga gaa gtg cag gat gtt ttg ata aaa atg ggt tac ccg cat	672
Leu Val Arg Glu Val Gln Asp Val Leu Ile Lys Met Gly Tyr Pro His	
210 215 220	
gct gaa gta tcc agc gaa ggg ccg ggg agc gtg tta att cat gat gat	720
Ala Glu Val Ser Ser Glu Gly Pro Gly Ser Val Leu Ile His Asp Asp	
225 230 235 240	
ata caa atg gat cag caa tgg cgc aag gtt caa cca tta ctt gca gat	768
Ile Gln Met Asp Gln Gln Trp Arg Lys Val Gln Pro Leu Leu Ala Asp	
245 250 255	
att ccc ggg tta ttg cac tgg cag att agt cac tct cat cag tct cag	816
Ile Pro Gly Leu Leu His Trp Gln Ile Ser His Ser His Gln Ser Gln	
260 265 270	
ggg gat gat att att tct gcg ata ata gag aac ggt tta gtg ggg ctt	864
Gly Asp Asp Ile Ile Ser Ala Ile Ile Glu Asn Gly Leu Val Gly Leu	
275 280 285	
gtc aat gtt agc cca atg cgg cgc tct ttt gtt atc agt ggt gta ctg	912
Val Asn Val Ser Pro Met Arg Arg Ser Phe Val Ile Ser Gly Val Leu	
290 295 300	
gat gaa tct cat caa cgc att ttg caa gaa acg tta gca gca tta aag	960
Asp Glu Ser His Gln Arg Ile Leu Gln Glu Thr Leu Ala Ala Leu Lys	
305 310 315 320	
aaa aag gat ccc gct ctt tct tta att tat cag gat att gcg cct tcc	1008
Lys Lys Asp Pro Ala Leu Ser Leu Ile Tyr Gln Asp Ile Ala Pro Ser	
325 330 335	
cat gat gaa agc aag tat ctg cct gcg cca gtg gct ggc ttt gta cag	1056
His Asp Glu Ser Lys Tyr Leu Pro Ala Pro Val Ala Gly Phe Val Gln	
340 345 350	
agt cgc cat ggt aat tac tta tta ctg acg aat aaa gag cgt tta cgt	1104
Ser Arg His Gly Asn Tyr Leu Leu Leu Thr Asn Lys Glu Arg Leu Arg	
355 360 365	
gta ggg gca ttg tta ccc aat ggg gga gaa att gtc cat ctg agt gcc	1152

Val Gly Ala Leu Leu Pro Asn Gly Gly Glu Ile Val His Leu Ser Ala
370 375 380

gat gtg gta acg att aaa cat tat gat act ttg att aac tat cca tta 1200
Asp Val Val Thr Ile Lys His Tyr Asp Thr Leu Ile Asn Tyr Pro Leu
385 390 395 400

gat ttt aag tga 1212
Asp Phe Lys

<210> 23

<211> 403

<212> PRT

<213> Salmonella

<400> 23

Met Ala Tyr Leu Met Val Asn Pro Lys Ser Ser Trp Lys Ile Arg Phe
1 5 10 15

Leu Gly His Val Leu Gln Gly Arg Glu Val Trp Leu Asn Glu Gly Asn
20 25 30

Leu Ser Leu Gly Glu Lys Gly Cys Asp Ile Cys Ile Pro Leu Ala Ile
35 40 45

Asn Glu Lys Ile Ile Leu Arg Glu Gln Ala Asp Ser Leu Phe Val Asp
50 55 60

Ala Gly Lys Ala Arg Val Arg Val Asn Gly Arg Arg Phe Asn Pro Asn
65 70 75 80

Lys Pro Leu Pro Ser Ser Gly Val Leu Gln Val Ala Gly Val Ala Ile
85 90 95

Ala Phe Gly Lys Gln Asp Cys Glu Leu Ala Asp Tyr Gln Ile Pro Val
100 105 110

Ser Arg Ser Gly Tyr Trp Trp Leu Ala Gly Val Phe Leu Ile Phe Ile
115 120 125

Gly Gly Met Gly Val Leu Leu Ser Ile Ser Gly Gln Pro Glu Thr Val
130 135 140

Asn Asp Leu Pro Leu Arg Val Lys Phe Leu Leu Asp Lys Ser Asn Ile
145 150 155 160

His Tyr Val Arg Ala Gln Trp Lys Glu Asp Gly Ser Leu Gln Leu Ser
165 170 175

Gly Tyr Cys Ser Ser Ser Glu Gln Met Gln Lys Val Arg Ala Thr Leu
180 185 190

Glu Ser Trp Gly Val Met Tyr Arg Asp Gly Val Ile Cys Asp Asp Leu
195 200 205

Leu Val Arg Glu Val Gln Asp Val Leu Ile Lys Met Gly Tyr Pro His

210						215						220					
Ala	Glu	Val	Ser	Ser	Glu	Gly	Pro	Gly	Ser	Val	Leu	Ile	His	Asp	Asp		
225					230					235					240		
Ile	Gln	Met	Asp	Gln	Gln	Trp	Arg	Lys	Val	Gln	Pro	Leu	Leu	Ala	Asp		
				245					250					255			
Ile	Pro	Gly	Leu	Leu	His	Trp	Gln	Ile	Ser	His	Ser	His	Gln	Ser	Gln		
			260					265					270				
Gly	Asp	Asp	Ile	Ile	Ser	Ala	Ile	Ile	Glu	Asn	Gly	Leu	Val	Gly	Leu		
		275					280					285					
Val	Asn	Val	Ser	Pro	Met	Arg	Arg	Ser	Phe	Val	Ile	Ser	Gly	Val	Leu		
	290					295					300						
Asp	Glu	Ser	His	Gln	Arg	Ile	Leu	Gln	Glu	Thr	Leu	Ala	Ala	Leu	Lys		
305				310						315					320		
Lys	Lys	Asp	Pro	Ala	Leu	Ser	Leu	Ile	Tyr	Gln	Asp	Ile	Ala	Pro	Ser		
				325					330					335			
His	Asp	Glu	Ser	Lys	Tyr	Leu	Pro	Ala	Pro	Val	Ala	Gly	Phe	Val	Gln		
			340					345					350				
Ser	Arg	His	Gly	Asn	Tyr	Leu	Leu	Leu	Thr	Asn	Lys	Glu	Arg	Leu	Arg		
		355					360					365					
Val	Gly	Ala	Leu	Leu	Pro	Asn	Gly	Gly	Glu	Ile	Val	His	Leu	Ser	Ala		
	370					375					380						
Asp	Val	Val	Thr	Ile	Lys	His	Tyr	Asp	Thr	Leu	Ile	Asn	Tyr	Pro	Leu		
385					390					395					400		
Asp	Phe	Lys															

<210> 24
 <211> 243
 <212> DNA
 <213> Salmonella

<220>
 <221> CDS
 <222> (1)..(240)

<400> 24																		
atg	aca	act	ttg	acc	cgg	tta	gaa	gat	ttg	ctg	ctt	cat	tcg	cgt	gaa			48
Met	Thr	Thr	Leu	Thr	Arg	Leu	Glu	Asp	Leu	Leu	Leu	His	Ser	Arg	Glu			
1				5					10					15				
gag	gcc	aaa	ggc	ata	att	tta	caa	tta	agg	gct	gcc	cgg	aaa	cag	tta			96
Glu	Ala	Lys	Gly	Ile	Ile	Leu	Gln	Leu	Arg	Ala	Ala	Arg	Lys	Gln	Leu			
			20					25						30				

cca gaa tcg atg att aaa gcg caa ttt gcc tta cag cag tat tct aca 144
Pro Glu Ser Met Ile Lys Ala Gln Phe Ala Leu Gln Gln Tyr Ser Thr
35 40 45

ttt att aat tac gaa agt tca ctg atc aaa atg atc aag gat atg ctt 192
Phe Ile Asn Tyr Glu Ser Ser Leu Ile Lys Met Ile Lys Asp Met Leu
50 55 60

agt gga atc att gct aaa atc tga 216
Ser Gly Ile Ile Ala Lys Ile
65 70

<210> 27
<211> 71
<212> PRT
<213> Salmonella

<400> 27
Met Asp Ile Ala Gln Leu Val Asp Met Leu Ser His Met Ala His Gln
1 5 10 15

Ala Gly Gln Ala Ile Asn Asp Lys Met Asn Gly Asn Asp Leu Leu Asn
20 25 30

Pro Glu Ser Met Ile Lys Ala Gln Phe Ala Leu Gln Gln Tyr Ser Thr
35 40 45

Phe Ile Asn Tyr Glu Ser Ser Leu Ile Lys Met Ile Lys Asp Met Leu
50 55 60

Ser Gly Ile Ile Ala Lys Ile
65 70

<210> 28
<211> 228
<212> DNA
<213> Salmonella

<220>
<221> CDS
<222> (1)..(225)

<400> 28
atg ttt gcg ggc gtt aac cat agc ctg att tcc cag gta cat gcg atg 48
Met Phe Ala Gly Val Asn His Ser Leu Ile Ser Gln Val His Ala Met
1 5 10 15

tta cca gcg cta acg gtt att gtt ccg gat aaa aaa tta cag ttg gta 96
Leu Pro Ala Leu Thr Val Ile Val Pro Asp Lys Lys Leu Gln Leu Val
20 25 30

tgt ctg gca tta ttg ttg gcg ggt tta aat gag ccg cta aaa gcc gcg 144
Cys Leu Ala Leu Leu Leu Ala Gly Leu Asn Glu Pro Leu Lys Ala Ala
35 40 45

aaa att tta tcg gat ata gat ttg cca gag gct atg gcg ctg cgt ctg 192
Lys Ile Leu Ser Asp Ile Asp Leu Pro Glu Ala Met Ala Leu Arg Leu
50 55 60

tta ttt cct gca cca aat gag ggg ttt gaa aat tga 228
Leu Phe Pro Ala Pro Asn Glu Gly Phe Glu Asn
65 70 75

<210> 29
<211> 75
<212> PRT
<213> Salmonella

<400> 29
Met Phe Ala Gly Val Asn His Ser Leu Ile Ser Gln Val His Ala Met
1 5 10 15

Leu Pro Ala Leu Thr Val Ile Val Pro Asp Lys Lys Leu Gln Leu Val
20 25 30

Cys Leu Ala Leu Leu Leu Ala Gly Leu Asn Glu Pro Leu Lys Ala Ala
35 40 45

Lys Ile Leu Ser Asp Ile Asp Leu Pro Glu Ala Met Ala Leu Arg Leu
50 55 60

Leu Phe Pro Ala Pro Asn Glu Gly Phe Glu Asn
65 70 75

<210> 30
<211> 249
<212> DNA
<213> Salmonella

<220>
<221> CDS
<222> (1)..(246)

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Met Ser Val Val Pro Val Ser Thr Gln Ser Tyr Val Lys Ser Ser Ala
1 5 10 15

gaa ccg agc cag gag caa att aat ttt ttt gaa caa ttg ctg aaa gat 96
Glu Pro Ser Gln Glu Gln Ile Asn Phe Phe Glu Gln Leu Leu Lys Asp
20 25 30

gaa gca tcc acc agt aac gcc agt gct tta tta ccg cag gtt atg ttg 144
Glu Ala Ser Thr Ser Asn Ala Ser Ala Leu Leu Pro Gln Val Met Leu
35 40 45

acc aga caa atg gat tat atg cag tta acg gta ggc gtc gat tat ctt 192
Thr Arg Gln Met Asp Tyr Met Gln Leu Thr Val Gly Val Asp Tyr Leu

50 55 60
gcc aga ata tca ggc gca gca tcg caa gcg ctt aat aag ctg gat aac 240
Ala Arg Ile Ser Gly Ala Ala Ser Gln Ala Leu Asn Lys Leu Asp Asn
65 70 75 80

atg gca tga 249
Met Ala

<210> 31
<211> 82
<212> PRT
<213> Salmonella

<400> 31
Met Ser Val Val Pro Val Ser Thr Gln Ser Tyr Val Lys Ser Ser Ala
1 5 10 15

Glu Pro Ser Gln Glu Gln Ile Asn Phe Phe Glu Gln Leu Leu Lys Asp
20 25 30

Glu Ala Ser Thr Ser Asn Ala Ser Ala Leu Leu Pro Gln Val Met Leu
35 40 45

Thr Arg Gln Met Asp Tyr Met Gln Leu Thr Val Gly Val Asp Tyr Leu
50 55 60

Ala Arg Ile Ser Gly Ala Ala Ser Gln Ala Leu Asn Lys Leu Asp Asn
65 70 75 80

Met Ala

<210> 32
<211> 750
<212> DNA
<213> Salmonella

<220>
<221> CDS
<222> (1)..(747)

<400> 32
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Met Lys Val His Arg Ile Val Phe Leu Thr Val Leu Thr Phe Phe Leu
1 5 10 15

acg gca tgt gat gtg gat ctt tat cgc tca ttg cca gaa gat gaa gcg 96
Thr Ala Cys Asp Val Asp Leu Tyr Arg Ser Leu Pro Glu Asp Glu Ala
20 25 30

aat caa atg ctg gca tta ctt atg cag cat cat att gat gcg gaa aaa 144
Asn Gln Met Leu Ala Leu Leu Met Gln His His Ile Asp Ala Glu Lys
35 40 45

aaa cag gaa gag gat ggt gta acc tta cgt gtc gag cag tcg cag ttt 192
 Lys Gln Glu Glu Asp Gly Val Thr Leu Arg Val Glu Gln Ser Gln Phe
 50 55 60

att aat gcg gtt gag cta ctt aga ctt aac ggt tat ccg cat agg cag 240
 Ile Asn Ala Val Glu Leu Leu Arg Leu Asn Gly Tyr Pro His Arg Gln
 65 70 75 80

ttt aca acg gcg gat aag atg ttt ccg gct aat cag tta gtg gta tca 288
 Phe Thr Thr Ala Asp Lys Met Phe Pro Ala Asn Gln Leu Val Val Ser
 85 90 95

ccc cag gaa gaa cag cag aag att aat ttt tta aaa gaa caa aga att 336
 Pro Gln Glu Glu Gln Gln Lys Ile Asn Phe Leu Lys Glu Gln Arg Ile
 100 105 110

gaa gga atg ctg agt cag atg gag ggc gtg att aat gca aaa gtg acc 384
 Glu Gly Met Leu Ser Gln Met Glu Gly Val Ile Asn Ala Lys Val Thr
 115 120 125

att gcg cta ccg act tat gat gag gga agt aac gct tct ccg agc tca 432
 Ile Ala Leu Pro Thr Tyr Asp Glu Gly Ser Asn Ala Ser Pro Ser Ser
 130 135 140

gtt gcc gta ttt ata aaa tat tca cct cag gtc aat atg gag gcc ttt 480
 Val Ala Val Phe Ile Lys Tyr Ser Pro Gln Val Asn Met Glu Ala Phe
 145 150 155 160

cgg gta aaa att aaa gat tta ata gag atg tca atc cct ggg ttg caa 528
 Arg Val Lys Ile Lys Asp Leu Ile Glu Met Ser Ile Pro Gly Leu Gln
 165 170 175

tac agt aag att agt atc ttg atg cag cct gct gaa ttc aga atg gta 576
 Tyr Ser Lys Ile Ser Ile Leu Met Gln Pro Ala Glu Phe Arg Met Val
 180 185 190

gct gac gta ccc gcg aga caa aca ttc tgg att atg gac gtt atc aac 624
 Ala Asp Val Pro Ala Arg Gln Thr Phe Trp Ile Met Asp Val Ile Asn
 195 200 205

gcc aat aaa ggg aag gtg gtg aag tgg ttg atg aaa tac cct tat ccg 672
 Ala Asn Lys Gly Lys Val Val Lys Trp Leu Met Lys Tyr Pro Tyr Pro
 210 215 220

ttg atg tta tcg ttg aca gga ctg tta tta gga gtg ggc atc ctg atc 720
 Leu Met Leu Ser Leu Thr Gly Leu Leu Leu Gly Val Gly Ile Leu Ile
 225 230 235 240

ggc tat ttt tgc ctg aga cgc cgt ttt tga 750
 Gly Tyr Phe Cys Leu Arg Arg Arg Phe
 245

<210> 33
 <211> 249
 <212> PRT

<213> Salmonella

<400> 33

Met Lys Val His Arg Ile Val Phe Leu Thr Val Leu Thr Phe Phe Leu
1 5 10 15
Thr Ala Cys Asp Val Asp Leu Tyr Arg Ser Leu Pro Glu Asp Glu Ala
20 25 30
Asn Gln Met Leu Ala Leu Leu Met Gln His His Ile Asp Ala Glu Lys
35 40 45
Lys Gln Glu Glu Asp Gly Val Thr Leu Arg Val Glu Gln Ser Gln Phe
50 55 60
Ile Asn Ala Val Glu Leu Leu Arg Leu Asn Gly Tyr Pro His Arg Gln
65 70 75 80
Phe Thr Thr Ala Asp Lys Met Phe Pro Ala Asn Gln Leu Val Val Ser
85 90 95
Pro Gln Glu Glu Gln Gln Lys Ile Asn Phe Leu Lys Glu Gln Arg Ile
100 105 110
Glu Gly Met Leu Ser Gln Met Glu Gly Val Ile Asn Ala Lys Val Thr
115 120 125
Ile Ala Leu Pro Thr Tyr Asp Glu Gly Ser Asn Ala Ser Pro Ser Ser
130 135 140
Val Ala Val Phe Ile Lys Tyr Ser Pro Gln Val Asn Met Glu Ala Phe
145 150 155 160
Arg Val Lys Ile Lys Asp Leu Ile Glu Met Ser Ile Pro Gly Leu Gln
165 170 175
Tyr Ser Lys Ile Ser Ile Leu Met Gln Pro Ala Glu Phe Arg Met Val
180 185 190
Ala Asp Val Pro Ala Arg Gln Thr Phe Trp Ile Met Asp Val Ile Asn
195 200 205
Ala Asn Lys Gly Lys Val Val Lys Trp Leu Met Lys Tyr Pro Tyr Pro
210 215 220
Leu Met Leu Ser Leu Thr Gly Leu Leu Leu Gly Val Gly Ile Leu Ile
225 230 235 240
Gly Tyr Phe Cys Leu Arg Arg Arg Phe
245

<210> 34

<211> 2763

<212> DNA

<213> Salmonella

<220>

<221> CDS

<222> (1)..(2760)

<400> 34

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Met Asn Leu Leu Asn Leu Lys Asn Thr Leu Gln Thr Ser Leu Val Ile	
1 5 10 15	
agg cta act ttt tta ttt tta tta aca aca ata att att tgg ctg cta	96
Arg Leu Thr Phe Leu Phe Leu Leu Thr Thr Ile Ile Ile Trp Leu Leu	
20 25 30	
tct gtg ctt acc gca gct tat ata tca atg gtt cag aaa cgg cag cat	144
Ser Val Leu Thr Ala Ala Tyr Ile Ser Met Val Gln Lys Arg Gln His	
35 40 45	
ata ata gag gat tta tcc gtt cta tcc gag atg aat att gta cta agc	192
Ile Ile Glu Asp Leu Ser Val Leu Ser Glu Met Asn Ile Val Leu Ser	
50 55 60	
aat caa cgg ttt gaa gaa gct gaa cgt gac gct aaa aat tta atg tat	240
Asn Gln Arg Phe Glu Glu Ala Glu Arg Asp Ala Lys Asn Leu Met Tyr	
65 70 75 80	
caa tgc tca tta gcg act gag att cat cat aac gat att ttc cct gag	288
Gln Cys Ser Leu Ala Thr Glu Ile His His Asn Asp Ile Phe Pro Glu	
85 90 95	
gtg agc cgg cat cta tct gtc ggt cct tca aat tgc acg ccg acg cta	336
Val Ser Arg His Leu Ser Val Gly Pro Ser Asn Cys Thr Pro Thr Leu	
100 105 110	
aac gga gag aag cac cgt ctc ttt ctg cag tcc tct gat atc gat gaa	384
Asn Gly Glu Lys His Arg Leu Phe Leu Gln Ser Ser Asp Ile Asp Glu	
115 120 125	
aat agc ttt cgt cgc gat agt ttt att ctt aat cat aaa aat gag att	432
Asn Ser Phe Arg Arg Asp Ser Phe Ile Leu Asn His Lys Asn Glu Ile	
130 135 140	
tcg tta tta tct act gat aac cct tca gat tat tca act cta cag cct	480
Ser Leu Leu Ser Thr Asp Asn Pro Ser Asp Tyr Ser Thr Leu Gln Pro	
145 150 155 160	
tta acg cga aaa agc ttt cct tta tac cca acc cat gcc ggg ttt tac	528
Leu Thr Arg Lys Ser Phe Pro Leu Tyr Pro Thr His Ala Gly Phe Tyr	
165 170 175	
tgg agt gaa cca gaa tac ata aac ggc aaa gga tgg cac gct tcc gtt	576
Trp Ser Glu Pro Glu Tyr Ile Asn Gly Lys Gly Trp His Ala Ser Val	
180 185 190	
gcg gtt gcc gat cag caa ggc gta ttt ttt gag gtg acg gtt aaa ctt	624
Ala Val Ala Asp Gln Gln Gly Val Phe Phe Glu Val Thr Val Lys Leu	
195 200 205	

ccc gat ctc att act aag agc cac ctg cca tta gat gat agt att cga	672
Pro Asp Leu Ile Thr Lys Ser His Leu Pro Leu Asp Asp Ser Ile Arg	
210 215 220	
gta tgg ctg gat caa aac aac cac tta ttg ccg ttt tca tac atc ccg	720
Val Trp Leu Asp Gln Asn Asn His Leu Leu Pro Phe Ser Tyr Ile Pro	
225 230 235 240	
caa aaa ata cgt aca cag tta gaa aat gta acg ctg cat gat gga tgg	768
Gln Lys Ile Arg Thr Gln Leu Glu Asn Val Thr Leu His Asp Gly Trp	
245 250 255	
cag caa att ccc gga ttt ctg ata tta cgc aca acc ttg cat ggc ccc	816
Gln Gln Ile Pro Gly Phe Leu Ile Leu Arg Thr Thr Leu His Gly Pro	
260 265 270	
gga tgg agt ctg gtt acg ctg tac cca tac ggt aat cta cat aat cgc	864
Gly Trp Ser Leu Val Thr Leu Tyr Pro Tyr Gly Asn Leu His Asn Arg	
275 280 285	
atc tta aaa att atc ctt caa caa atc ccc ttt aca tta aca gca ttg	912
Ile Leu Lys Ile Ile Leu Gln Gln Ile Pro Phe Thr Leu Thr Ala Leu	
290 295 300	
gtg ttg atg acg tcg gct ttt tgc tgg tta cta cat cgc tca ctg gcc	960
Val Leu Met Thr Ser Ala Phe Cys Trp Leu Leu His Arg Ser Leu Ala	
305 310 315 320	
aaa ccg tta tgg cgt ttt gtc gat gtc att aat aaa acc gca act gca	1008
Lys Pro Leu Trp Arg Phe Val Asp Val Ile Asn Lys Thr Ala Thr Ala	
325 330 335	
ccg ctg agc aca cgt tta cca gca caa cga ctg gat gaa tta gat agt	1056
Pro Leu Ser Thr Arg Leu Pro Ala Gln Arg Leu Asp Glu Leu Asp Ser	
340 345 350	
att gcc ggt gct ttt aac caa ctg ctt gat act cta caa gtc caa tac	1104
Ile Ala Gly Ala Phe Asn Gln Leu Leu Asp Thr Leu Gln Val Gln Tyr	
355 360 365	
gac aat ctg gaa aac aaa gtc gca gag cgc acc cag gcg cta aat gaa	1152
Asp Asn Leu Glu Asn Lys Val Ala Glu Arg Thr Gln Ala Leu Asn Glu	
370 375 380	
gca aaa aaa cgc gct gag cga gct aac aaa cgt aaa agc att cat ctt	1200
Ala Lys Lys Arg Ala Glu Arg Ala Asn Lys Arg Lys Ser Ile His Leu	
385 390 395 400	
acg gta ata agt cat gag tta cgt act ccg atg aat ggc gta ctc ggt	1248
Thr Val Ile Ser His Glu Leu Arg Thr Pro Met Asn Gly Val Leu Gly	
405 410 415	
gca att gaa tta tta caa acc acc cct tta aac ata gag caa caa gga	1296
Ala Ile Glu Leu Leu Gln Thr Thr Pro Leu Asn Ile Glu Gln Gln Gly	
420 425 430	

tta gct gat acc gcc aga aat tgt aca ctg tct ttg tta gct att att	1344
Leu Ala Asp Thr Ala Arg Asn Cys Thr Leu Ser Leu Leu Ala Ile Ile	
435 440 445	
aat aat ctg ctg gat ttt tca cgc atc gag tct ggt cat ttc aca tta	1392
Asn Asn Leu Leu Asp Phe Ser Arg Ile Glu Ser Gly His Phe Thr Leu	
450 455 460	
cat atg gaa gaa aca gcg tta ctg ccg tta ctg gac cag gca atg caa	1440
His Met Glu Glu Thr Ala Leu Leu Pro Leu Leu Asp Gln Ala Met Gln	
465 470 475 480	
acc atc cag ggg cca gcg caa agc aaa aaa ctg tca tta cgt act ttt	1488
Thr Ile Gln Gly Pro Ala Gln Ser Lys Lys Leu Ser Leu Arg Thr Phe	
485 490 495	
gtc ggt caa cat gtc cct ctc tat ttt cat acc gac agt atc cgt tta	1536
Val Gly Gln His Val Pro Leu Tyr Phe His Thr Asp Ser Ile Arg Leu	
500 505 510	
cgg caa att ttg gtt aat tta ctc ggg aac gcg gta aaa ttt acc gaa	1584
Arg Gln Ile Leu Val Asn Leu Leu Gly Asn Ala Val Lys Phe Thr Glu	
515 520 525	
acc gga ggg ata cgt ctg acg gtc aag cgt cat gag gaa caa tta ata	1632
Thr Gly Gly Ile Arg Leu Thr Val Lys Arg His Glu Glu Gln Leu Ile	
530 535 540	
ttt ctg gtt agc gat agc ggt aaa ggg att gaa ata cag cag cag tct	1680
Phe Leu Val Ser Asp Ser Gly Lys Gly Ile Glu Ile Gln Gln Gln Ser	
545 550 555 560	
caa atc ttt act gct ttt tat caa gca gac aca aat tcg caa ggt aca	1728
Gln Ile Phe Thr Ala Phe Tyr Gln Ala Asp Thr Asn Ser Gln Gly Thr	
565 570 575	
gga att gga ctg act att gcg tca agc ctg gct aaa atg atg ggc ggt	1776
Gly Ile Gly Leu Thr Ile Ala Ser Ser Leu Ala Lys Met Met Gly Gly	
580 585 590	
aat ctg aca cta aaa agt gtc ccc ggg gtt gga acc tgt gtc tcg cta	1824
Asn Leu Thr Leu Lys Ser Val Pro Gly Val Gly Thr Cys Val Ser Leu	
595 600 605	
gta tta ccc tta caa gaa tac cag ccg cct caa cca att aaa ggg acg	1872
Val Leu Pro Leu Gln Glu Tyr Gln Pro Pro Gln Pro Ile Lys Gly Thr	
610 615 620	
ctg tca gcg ccg ttc tgc ctg cat cgg caa ctg gct tgc tgg gga ata	1920
Leu Ser Ala Pro Phe Cys Leu His Arg Gln Leu Ala Cys Trp Gly Ile	
625 630 635 640	
cgc ggt gaa cca ccc cac cag caa aat gcg ctt ctc aac gca gag ctt	1968
Arg Gly Glu Pro Pro His Gln Gln Asn Ala Leu Leu Asn Ala Glu Leu	
645 650 655	
ttg tat ttc tcc gga aaa ctc tac gac ctg gcg caa cag tta ata ttg	2016

Leu Tyr Phe Ser Gly Lys Leu Tyr Asp Leu Ala Gln Gln Leu Ile Leu	
660	665 670
tgt aca cca aat atg cca gta ata aat aat ttg tta cca ccc tgg cag	2064
Cys Thr Pro Asn Met Pro Val Ile Asn Asn Leu Leu Pro Pro Trp Gln	
675	680 685
ttg cag att ctt ttg gtt gat gat gcc gat att aat cgg gat atc atc	2112
Leu Gln Ile Leu Leu Val Asp Asp Ala Asp Ile Asn Arg Asp Ile Ile	
690	695 700
ggc aaa atg ctt gtc agc ctg ggc caa cac gtc act att gcc gcc agt	2160
Gly Lys Met Leu Val Ser Leu Gly Gln His Val Thr Ile Ala Ala Ser	
705	710 715 720
agt aac gag gct ctg act tta tca caa cag cag cga ttc gat tta gta	2208
Ser Asn Glu Ala Leu Thr Leu Ser Gln Gln Gln Arg Phe Asp Leu Val	
725	730 735
ctg att gac att aga atg cca gaa ata gat ggt att gaa tgt gta cga	2256
Leu Ile Asp Ile Arg Met Pro Glu Ile Asp Gly Ile Glu Cys Val Arg	
740	745 750
tta tgg cat gat gag ccg aat aat tta gat cct gac tgc atg ttt gtg	2304
Leu Trp His Asp Glu Pro Asn Asn Leu Asp Pro Asp Cys Met Phe Val	
755	760 765
gca cta tcc gct agc gta gcg aca gaa gat att cat cgt tgt aaa aaa	2352
Ala Leu Ser Ala Ser Val Ala Thr Glu Asp Ile His Arg Cys Lys Lys	
770	775 780
aat ggg att cat cat tac att aca aaa cca gtg aca ttg gct acc tta	2400
Asn Gly Ile His His Tyr Ile Thr Lys Pro Val Thr Leu Ala Thr Leu	
785	790 795 800
gct cgc tac atc agt att gcc gca gaa tac caa ctt tta cga aat ata	2448
Ala Arg Tyr Ile Ser Ile Ala Ala Glu Tyr Gln Leu Leu Arg Asn Ile	
805	810 815
gag cta cag gag cag gat ccg agt cgc tgc tca gcg cta ctg gcg aca	2496
Glu Leu Gln Glu Gln Asp Pro Ser Arg Cys Ser Ala Leu Leu Ala Thr	
820	825 830
gat gat atg gtc att aat agc aag att ttc caa tca ctg gac ctc ttg	2544
Asp Asp Met Val Ile Asn Ser Lys Ile Phe Gln Ser Leu Asp Leu Leu	
835	840 845
ctg gct gat att gaa aat gcc gta tcg gct gga gaa aaa atc gat cag	2592
Leu Ala Asp Ile Glu Asn Ala Val Ser Ala Gly Glu Lys Ile Asp Gln	
850	855 860
tta att cac aca tta aaa ggc tgt tta ggt caa ata ggg cag act gaa	2640
Leu Ile His Thr Leu Lys Gly Cys Leu Gly Gln Ile Gly Gln Thr Glu	
865	870 875 880
ttg gta tgc tat gtc ata gac att gag aat cgc gta aaa atg ggg aaa	2688
Leu Val Cys Tyr Val Ile Asp Ile Glu Asn Arg Val Lys Met Gly Lys	

885 890 895
atc atc gcg ctg gag gaa cta acc gac tta cgc cag aaa ata cgt atg 2736
Ile Ile Ala Leu Glu Glu Leu Thr Asp Leu Arg Gln Lys Ile Arg Met
 900 905 910

atc ttc aaa aac tac acc att act taa 2763
Ile Phe Lys Asn Tyr Thr Ile Thr
 915 920

<210> 35
<211> 920
<212> PRT
<213> Salmonella

<400> 35
Met Asn Leu Leu Asn Leu Lys Asn Thr Leu Gln Thr Ser Leu Val Ile
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Arg Leu Thr Phe Leu Phe Leu Leu Thr Thr Ile Ile Ile Trp Leu Leu
 20 25 30

Ser Val Leu Thr Ala Ala Tyr Ile Ser Met Val Gln Lys Arg Gln His
 35 40 45

Ile Ile Glu Asp Leu Ser Val Leu Ser Glu Met Asn Ile Val Leu Ser
 50 55 60

Asn Gln Arg Phe Glu Glu Ala Glu Arg Asp Ala Lys Asn Leu Met Tyr
 65 70 75 80

Gln Cys Ser Leu Ala Thr Glu Ile His His Asn Asp Ile Phe Pro Glu
 85 90 95

Val Ser Arg His Leu Ser Val Gly Pro Ser Asn Cys Thr Pro Thr Leu
 100 105 110

Asn Gly Glu Lys His Arg Leu Phe Leu Gln Ser Ser Asp Ile Asp Glu
 115 120 125

Asn Ser Phe Arg Arg Asp Ser Phe Ile Leu Asn His Lys Asn Glu Ile
 130 135 140

Ser Leu Leu Ser Thr Asp Asn Pro Ser Asp Tyr Ser Thr Leu Gln Pro
 145 150 155 160

Leu Thr Arg Lys Ser Phe Pro Leu Tyr Pro Thr His Ala Gly Phe Tyr
 165 170 175

Trp Ser Glu Pro Glu Tyr Ile Asn Gly Lys Gly Trp His Ala Ser Val
 180 185 190

Ala Val Ala Asp Gln Gln Gly Val Phe Phe Glu Val Thr Val Lys Leu
 195 200 205

Pro Asp Leu Ile Thr Lys Ser His Leu Pro Leu Asp Asp Ser Ile Arg

210						215										220
Val	Trp	Leu	Asp	Gln	Asn	Asn	His	Leu	Leu	Pro	Phe	Ser	Tyr	Ile	Pro	
225					230					235					240	
Gln	Lys	Ile	Arg	Thr	Gln	Leu	Glu	Asn	Val	Thr	Leu	His	Asp	Gly	Trp	
				245					250					255		
Gln	Gln	Ile	Pro	Gly	Phe	Leu	Ile	Leu	Arg	Thr	Thr	Leu	His	Gly	Pro	
			260					265					270			
Gly	Trp	Ser	Leu	Val	Thr	Leu	Tyr	Pro	Tyr	Gly	Asn	Leu	His	Asn	Arg	
		275					280					285				
Ile	Leu	Lys	Ile	Ile	Leu	Gln	Gln	Ile	Pro	Phe	Thr	Leu	Thr	Ala	Leu	
	290					295					300					
Val	Leu	Met	Thr	Ser	Ala	Phe	Cys	Trp	Leu	Leu	His	Arg	Ser	Leu	Ala	
305					310						315				320	
Lys	Pro	Leu	Trp	Arg	Phe	Val	Asp	Val	Ile	Asn	Lys	Thr	Ala	Thr	Ala	
				325					330					335		
Pro	Leu	Ser	Thr	Arg	Leu	Pro	Ala	Gln	Arg	Leu	Asp	Glu	Leu	Asp	Ser	
			340					345					350			
Ile	Ala	Gly	Ala	Phe	Asn	Gln	Leu	Leu	Asp	Thr	Leu	Gln	Val	Gln	Tyr	
		355					360					365				
Asp	Asn	Leu	Glu	Asn	Lys	Val	Ala	Glu	Arg	Thr	Gln	Ala	Leu	Asn	Glu	
	370					375					380					
Ala	Lys	Lys	Arg	Ala	Glu	Arg	Ala	Asn	Lys	Arg	Lys	Ser	Ile	His	Leu	
385					390					395					400	
Thr	Val	Ile	Ser	His	Glu	Leu	Arg	Thr	Pro	Met	Asn	Gly	Val	Leu	Gly	
				405					410					415		
Ala	Ile	Glu	Leu	Leu	Gln	Thr	Thr	Pro	Leu	Asn	Ile	Glu	Gln	Gln	Gly	
			420					425					430			
Leu	Ala	Asp	Thr	Ala	Arg	Asn	Cys	Thr	Leu	Ser	Leu	Leu	Ala	Ile	Ile	
		435					440					445				
Asn	Asn	Leu	Leu	Asp	Phe	Ser	Arg	Ile	Glu	Ser	Gly	His	Phe	Thr	Leu	
	450					455					460					
His	Met	Glu	Glu	Thr	Ala	Leu	Leu	Pro	Leu	Leu	Asp	Gln	Ala	Met	Gln	
465					470						475				480	
Thr	Ile	Gln	Gly	Pro	Ala	Gln	Ser	Lys	Lys	Leu	Ser	Leu	Arg	Thr	Phe	
				485					490					495		
Val	Gly	Gln	His	Val	Pro	Leu	Tyr	Phe	His	Thr	Asp	Ser	Ile	Arg	Leu	
			500					505					510			
Arg	Gln	Ile	Leu	Val	Asn	Leu	Leu	Gly	Asn	Ala	Val	Lys	Phe	Thr	Glu	

	515		520		525														
Thr	Gly	Gly	Ile	Arg	Leu	Thr	Val	Lys	Arg	His	Glu	Glu	Gln	Leu	Ile				
	530					535					540								
Phe	Leu	Val	Ser	Asp	Ser	Gly	Lys	Gly	Ile	Glu	Ile	Gln	Gln	Gln	Ser				
545					550					555					560				
Gln	Ile	Phe	Thr	Ala	Phe	Tyr	Gln	Ala	Asp	Thr	Asn	Ser	Gln	Gly	Thr				
				565					570					575					
Gly	Ile	Gly	Leu	Thr	Ile	Ala	Ser	Ser	Leu	Ala	Lys	Met	Met	Gly	Gly				
			580					585					590						
Asn	Leu	Thr	Leu	Lys	Ser	Val	Pro	Gly	Val	Gly	Thr	Cys	Val	Ser	Leu				
		595					600					605							
Val	Leu	Pro	Leu	Gln	Glu	Tyr	Gln	Pro	Pro	Gln	Pro	Ile	Lys	Gly	Thr				
	610					615					620								
Leu	Ser	Ala	Pro	Phe	Cys	Leu	His	Arg	Gln	Leu	Ala	Cys	Trp	Gly	Ile				
625					630					635					640				
Arg	Gly	Glu	Pro	Pro	His	Gln	Gln	Asn	Ala	Leu	Leu	Asn	Ala	Glu	Leu				
				645					650					655					
Leu	Tyr	Phe	Ser	Gly	Lys	Leu	Tyr	Asp	Leu	Ala	Gln	Gln	Leu	Ile	Leu				
			660					665					670						
Cys	Thr	Pro	Asn	Met	Pro	Val	Ile	Asn	Asn	Leu	Leu	Pro	Pro	Trp	Gln				
		675					680					685							
Leu	Gln	Ile	Leu	Leu	Val	Asp	Asp	Ala	Asp	Ile	Asn	Arg	Asp	Ile	Ile				
	690					695					700								
Gly	Lys	Met	Leu	Val	Ser	Leu	Gly	Gln	His	Val	Thr	Ile	Ala	Ala	Ser				
705					710					715					720				
Ser	Asn	Glu	Ala	Leu	Thr	Leu	Ser	Gln	Gln	Gln	Arg	Phe	Asp	Leu	Val				
				725					730					735					
Leu	Ile	Asp	Ile	Arg	Met	Pro	Glu	Ile	Asp	Gly	Ile	Glu	Cys	Val	Arg				
			740					745					750						
Leu	Trp	His	Asp	Glu	Pro	Asn	Asn	Leu	Asp	Pro	Asp	Cys	Met	Phe	Val				
	755						760					765							
Ala	Leu	Ser	Ala	Ser	Val	Ala	Thr	Glu	Asp	Ile	His	Arg	Cys	Lys	Lys				
	770					775					780								
Asn	Gly	Ile	His	His	Tyr	Ile	Thr	Lys	Pro	Val	Thr	Leu	Ala	Thr	Leu				
785					790					795					800				
Ala	Arg	Tyr	Ile	Ser	Ile	Ala	Ala	Glu	Tyr	Gln	Leu	Leu	Arg	Asn	Ile				
				805					810					815					
Glu	Leu	Gln	Glu	Gln	Asp	Pro	Ser	Arg	Cys	Ser	Ala	Leu	Leu	Ala	Thr				

	820		825		830												
Asp	Asp	Met	Val	Ile	Asn	Ser	Lys	Ile	Phe	Gln	Ser	Leu	Asp	Leu	Leu		
	835						840					845					
Leu	Ala	Asp	Ile	Glu	Asn	Ala	Val	Ser	Ala	Gly	Glu	Lys	Ile	Asp	Gln		
	850					855					860						
Leu	Ile	His	Thr	Leu	Lys	Gly	Cys	Leu	Gly	Gln	Ile	Gly	Gln	Thr	Glu		
865					870					875					880		
Leu	Val	Cys	Tyr	Val	Ile	Asp	Ile	Glu	Asn	Arg	Val	Lys	Met	Gly	Lys		
				885					890					895			
Ile	Ile	Ala	Leu	Glu	Glu	Leu	Thr	Asp	Leu	Arg	Gln	Lys	Ile	Arg	Met		
			900					905						910			
Ile	Phe	Lys	Asn	Tyr	Thr	Ile	Thr										
		915					920										

<210> 36
 <211> 639
 <212> DNA
 <213> Salmonella

<220>
 <221> CDS
 <222> (1)..(636)

<400> 36
 atg aaa gaa tat aag atc tta tta gta gac gat cat gaa atc atc att 48
 Met Lys Glu Tyr Lys Ile Leu Leu Val Asp Asp His Glu Ile Ile Ile
 1 5 10 15
 aac ggc att atg aat gcc tta tta ccc tgg cct cat ttt aaa att gta 96
 Asn Gly Ile Met Asn Ala Leu Leu Pro Trp Pro His Phe Lys Ile Val
 20 25 30
 gag cat gtt aaa aat ggt ctt gag gtt tat aat gcc tgt tgt gca tac 144
 Glu His Val Lys Asn Gly Leu Glu Val Tyr Asn Ala Cys Cys Ala Tyr
 35 40 45
 gag cct gac ata ctt atc ctt gat ctt agt cta cct ggc atc aat ggc 192
 Glu Pro Asp Ile Leu Ile Leu Asp Leu Ser Leu Pro Gly Ile Asn Gly
 50 55 60
 ctg gat atc att cct caa tta cat cag cgt tgg cca gca atg aat att 240
 Leu Asp Ile Ile Pro Gln Leu His Gln Arg Trp Pro Ala Met Asn Ile
 65 70 75 80
 ctg gtt tac aca gca tac caa caa gag tat atg acc att aaa act tta 288
 Leu Val Tyr Thr Ala Tyr Gln Gln Glu Tyr Met Thr Ile Lys Thr Leu
 85 90 95
 gcc gca ggt gct aat ggc tat gtt tta aaa agc agt agt cag caa gtt 336

Ala Ala Gly Ala Asn Gly Tyr Val Leu Lys Ser Ser Ser Gln Gln Val
100 105 110

ctg tta gcg gca ttg caa aca gta gca gta aac aag cgt tac att gac 384
Leu Leu Ala Ala Leu Gln Thr Val Ala Val Asn Lys Arg Tyr Ile Asp
115 120 125

cca acg ttg aat cgg gaa gct atc ctg gct gaa tta aac gct gac acg 432
Pro Thr Leu Asn Arg Glu Ala Ile Leu Ala Glu Leu Asn Ala Asp Thr
130 135 140

acc aat cat caa ctg ctt act ttg cgc gag cgt cag gtt ctt aaa ctt 480
Thr Asn His Gln Leu Leu Thr Leu Arg Glu Arg Gln Val Leu Lys Leu
145 150 155 160

att gac gag ggg tat acc aat cat ggg atc agc gaa aag cta cat atc 528
Ile Asp Glu Gly Tyr Thr Asn His Gly Ile Ser Glu Lys Leu His Ile
165 170 175

agt ata aaa acc gtc gaa aca cac cgg atg aat atg atg aga aag cta 576
Ser Ile Lys Thr Val Glu Thr His Arg Met Asn Met Met Arg Lys Leu
180 185 190

cag gtt cat aaa gtg aca gag tta ctt aac tgt gcc cga aga atg agg 624
Gln Val His Lys Val Thr Glu Leu Leu Asn Cys Ala Arg Arg Met Arg
195 200 205

tta ata gag tat taa 639
Leu Ile Glu Tyr
210

<210> 37
<211> 212
<212> PRT
<213> Salmonella

<400> 37
Met Lys Glu Tyr Lys Ile Leu Leu Val Asp Asp His Glu Ile Ile Ile
1 5 10 15

Asn Gly Ile Met Asn Ala Leu Leu Pro Trp Pro His Phe Lys Ile Val
20 25 30

Glu His Val Lys Asn Gly Leu Glu Val Tyr Asn Ala Cys Cys Ala Tyr
35 40 45

Glu Pro Asp Ile Leu Ile Leu Asp Leu Ser Leu Pro Gly Ile Asn Gly
50 55 60

Leu Asp Ile Ile Pro Gln Leu His Gln Arg Trp Pro Ala Met Asn Ile
65 70 75 80

Leu Val Tyr Thr Ala Tyr Gln Gln Glu Tyr Met Thr Ile Lys Thr Leu
85 90 95

Ala Ala Gly Ala Asn Gly Tyr Val Leu Lys Ser Ser Ser Gln Gln Val

	100		105		110										
Leu	Leu	Ala	Ala	Leu	Gln	Thr	Val	Ala	Val	Asn	Lys	Arg	Tyr	Ile	Asp
		115					120					125			
Pro	Thr	Leu	Asn	Arg	Glu	Ala	Ile	Leu	Ala	Glu	Leu	Asn	Ala	Asp	Thr
	130					135					140				
Thr	Asn	His	Gln	Leu	Leu	Thr	Leu	Arg	Glu	Arg	Gln	Val	Leu	Lys	Leu
145					150					155					160
Ile	Asp	Glu	Gly	Tyr	Thr	Asn	His	Gly	Ile	Ser	Glu	Lys	Leu	His	Ile
				165					170					175	
Ser	Ile	Lys	Thr	Val	Glu	Thr	His	Arg	Met	Asn	Met	Met	Arg	Lys	Leu
			180					185						190	
Gln	Val	His	Lys	Val	Thr	Glu	Leu	Leu	Asn	Cys	Ala	Arg	Arg	Met	Arg
		195					200							205	
Leu	Ile	Glu	Tyr												
	210														

<210> 38
 <211> 388
 <212> DNA
 <213> Salmonella

<400> 38
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 agtttcacga gaagattaat cgatggtggt atcattagga agataaattt cttcatatat 120
 aaccagtcg atgactacaa ttacttttta ataagatggc gatgtaaaaa catcgtaca 180
 gtttatttaa taaataattt ttcaaattgt aagtttttat gtcaatgctg aaaatgtaat 240
 tgtgaattta tcggaaaatc cgaatgatag aatcgctgt gacaaggat atgtagacag 300
 catcctgata ttgtacaaga agagatagtc gaaataaatg tgaatcaggc tttttacgga 360
 tgtggtgtg agcgaatttg atagaaac 388

<210> 39
 <211> 262
 <212> DNA
 <213> Salmonella

<400> 39
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 atagcgcgca aaaaccgag cgtagacgta gtacgtgagg tttgactcgc tacgctcgcc 120
 cttcgggccc ccgctagcgg cgttcaaaac gctaacgcgt tttggcgagc actgcccagg 180
 ttcaaatgg caagtaaaat agcctaattg gataggctct tagttagcac gttaattatc 240
 tatcgtgtat atggaggga at 262

<210> 40
 <211> 192
 <212> PRT
 <213> EPEC

<300>

<303> Mol. Microbiol.

<304> 28

<306> 1-4

<307> 1998

<400> 40

Met Asp Thr Ser Thr Thr Ala Ser Val Ala Ser Ala Asn Ala Ser Thr
1 5 10 15

Ser Thr Ser Met Ala Tyr Asp Leu Gly Ser Met Ser Lys Asp Asp Val
20 25 30

Ile Asp Leu Phe Asn Lys Leu Gly Val Phe Gln Ala Ala Ile Leu Met
35 40 45

Phe Ala Tyr Met Tyr Gln Ala Gln Ser Asp Leu Ser Ile Ala Lys Phe
50 55 60

Ala Asp Met Asn Glu Ala Ser Lys Glu Ser Thr Thr Ala Gln Lys Met
65 70 75 80

Ala Asn Leu Val Asp Ala Lys Ile Ala Asp Val Gln Ser Ser Ser Asp
85 90 95

Lys Asn Ala Lys Ala Gln Leu Pro Asp Glu Val Ile Ser Tyr Ile Asn
100 105 110

Asp Pro Arg Asn Asp Ile Thr Ile Ser Gly Ile Asp Asn Ile Asn Ala
115 120 125

Gln Leu Gly Ala Gly Asp Leu Gln Thr Val Lys Ala Ala Ile Ser Ala
130 135 140

Lys Ala Asn Asn Leu Thr Thr Thr Val Asn Asn Ser Gln Leu Glu Ile
145 150 155 160

Gln Gln Met Ser Asn Thr Leu Asn Leu Leu Thr Ser Ala Arg Ser Asp
165 170 175

Met Gln Ser Leu Gln Tyr Arg Thr Ile Ser Gly Ile Ser Leu Gly Lys
180 185 190

<210> 41

<211> 380

<212> PRT

<213> EPEC

<300>

<303> Mol. Microbiol.

<304> 28

<306> 1-4
<307> 1998

<400> 41

Met Leu Asn Val Asn Asn Asp Ile Gln Ser Val Arg Ser Gly Ala Ser
1 5 10 15

Ala Ala Thr Ala Thr Ser Gly Ile Asn Gln Ser Glu Val Thr Ser Ala
20 25 30

Leu Asp Leu Gln Leu Val Lys Ser Thr Ala Pro Ser Ala Ser Trp Thr
35 40 45

Glu Ser Thr Ala Leu Ala Thr Pro Pro Ala Gly His Ser Leu Val Thr
50 55 60

Pro Ser Ala Ala Glu Asp Val Leu Ser Lys Leu Phe Gly Gly Ile Ser
65 70 75 80

Gly Glu Val Thr Ser Arg Thr Glu Gly Thr Glu Pro Gln Arg Ser Thr
85 90 95

Gln Asn Ala Ser Ser Gly Tyr Pro Tyr Leu Ser Gln Val Asn Asn Val
100 105 110

Asp Pro Gln Ala Met Met Met Met Ala Thr Leu Leu Ser Leu Asp Ala
115 120 125

Ser Ala Gln Arg Val Ala Ser Met Lys Asn Ser Asn Glu Ile Tyr Ala
130 135 140

Asp Gly Gln Asn Lys Ala Leu Asp Asn Lys Thr Leu Glu Phe Lys Lys
145 150 155 160

Gln Leu Glu Glu Gln Gln Lys Ala Glu Glu Lys Ala Gln Lys Ser Lys
165 170 175

Ile Val Gly Gln Val Phe Gly Trp Leu Gly Val Ala Ala Thr Ala Ile
180 185 190

Ala Ala Ile Phe Asn Pro Ala Leu Trp Ala Val Val Ala Ile Ser Ala
195 200 205

Thr Ala Met Ala Leu Gln Thr Ala Val Asp Val Met Gly Asp Asp Ala
210 215 220

Pro Gln Ala Leu Lys Thr Ala Ala Gln Ala Phe Gly Gly Leu Ser Leu
225 230 235 240

Ala Ala Gly Ile Leu Thr Ala Gly Ile Gly Gly Val Ser Ser Leu Ile
245 250 255

Ser Lys Val Gly Asp Val Ala Asn Lys Val Gly Ser Asn Ile Val Lys
260 265 270

Val Val Thr Thr Leu Ala Asp Thr Phe Val Asp Asn Val Ala Ser Lys
275 280 285

Ile Ser Ala Val Ala Asn Gly Leu Thr Thr Ser Ser Arg Ser Ile Gly
 290 295 300

Thr Thr Val Leu Asn Asn Asp Ala Ala Tyr Tyr Asn Val Leu Ser Gln
 305 310 315 320

Val Ser Ala Phe Ala Val Glu Asn Leu Thr Arg Gln Ser Glu Tyr Leu
 325 330 335

Ser Gln Ser Ala Lys Ala Glu Leu Glu Lys Ala Thr Leu Glu Leu Gln
 340 345 350

Asn Gln Ala Asn Tyr Ile Gln Ser Ala Ser Gln Leu Met Ser Asp Ser
 355 360 365

Ala Arg Val Asn Ile Arg Ile Val Ser Gly Arg Val
 370 375 380

<210> 42
 <211> 401
 <212> PRT
 <213> Yersinia enterocolitica

<300>
 <301> Hakansson, S.
 Schesser, K.
 Persson, C.
 Galyov, E. E.
 Rosqvist, R.
 Homble, F.
 Wolf Watz, H.
 <303> EMBO J.
 <304> 15
 <306> 5812-5823
 <307> 1996

<400> 42
 Met Ser Ala Leu Ile Thr His Asp Arg Ser Thr Pro Val Thr Gly Ser
 1 5 10 15

Leu Val Pro Tyr Ile Glu Thr Pro Ala Pro Ala Pro Leu Gln Thr Gln
 20 25 30

Gln Val Ala Gly Glu Leu Lys Asp Lys Asn Gly Gly Val Ser Ser Gln
 35 40 45

Gly Val Gln Leu Pro Ala Pro Leu Ala Val Val Ala Ser Gln Val Thr
 50 55 60

Glu Gly Gln Gln Gln Glu Ile Thr Lys Leu Leu Glu Ser Val Thr Arg
 65 70 75 80

Gly Thr Ala Gly Ser Gln Leu Ile Ser Asn Tyr Val Ser Val Leu Thr
 85 90 95

Asn Phe Thr Leu Ala Ser Pro Asp Thr Phe Glu Ile Glu Leu Gly Lys
 100 105 110

Leu Val Ser Asn Leu Glu Glu Val Arg Lys Asp Ile Lys Ile Ala Asp
 115 120 125

Ile Gln Arg Leu His Glu Gln Asn Met Lys Lys Ile Glu Glu Asn Gln
 130 135 140

Glu Lys Ile Lys Glu Thr Glu Glu Asn Ala Lys Gln Val Lys Lys Ser
 145 150 155 160

Gly Met Ala Ser Lys Ile Phe Gly Trp Leu Ile Ala Ile Ala Ser Val
 165 170 175

Val Ile Gly Ala Ile Met Val Ala Ser Gly Val Gly Ala Val Ala Gly
 180 185 190

Ala Met Met Ile Ala Ser Gly Val Ile Gly Met Ala Asn Met Ala Val
 195 200 205

Lys Gln Ala Ala Glu Asp Gly Leu Ile Ser Gln Glu Ala Met Gln Val
 210 215 220

Leu Gly Pro Ile Leu Thr Ala Ile Glu Val Ala Leu Thr Val Val Ser
 225 230 235 240

Thr Val Met Thr Phe Gly Gly Ser Ala Leu Lys Cys Leu Ala Asp Ile
 245 250 255

Gly Ala Lys Leu Gly Ala Asn Thr Ala Ser Leu Ala Ala Lys Gly Ala
 260 265 270

Glu Phe Ser Ala Lys Val Ala Gln Ile Ser Thr Gly Ile Ser Asn Thr
 275 280 285

Val Gly Ser Ala Val Thr Lys Leu Gly Gly Ser Phe Gly Ser Leu Thr
 290 295 300

Met Ser His Val Ile Arg Thr Gly Ser Gln Ala Thr Gln Val Ala Val
 305 310 315 320

Gly Val Gly Ser Gly Ile Thr Gln Thr Ile Asn Asn Lys Lys Gln Ala
 325 330 335

Asp Leu Gln His Asn Asn Ala Asp Leu Ala Leu Asn Lys Ala Asp Met
 340 345 350

Ala Ala Leu Gln Ser Ile Ile Asp Arg Leu Lys Glu Glu Leu Ser His
 355 360 365

Leu Ser Glu Ser His Arg Gln Val Met Glu Leu Ile Phe Gln Met Ile
 370 375 380

Asn Ala Lys Gly Asp Met Leu His Asn Leu Ala Gly Arg Pro His Thr
 385 390 395 400

Val

<210> 43
<211> 390
<212> PRT
<213> Pseudomonas aeruginosa

<300>
<301> Hauser, A. R.
Fleiszig, S.
Kang, P. J.
Mostov, K.
Engel, J. N.
<303> Infect. Immun.
<304> 66
<306> 1413-1420
<307> 1998

<400> 43
Met Asn Pro Ile Thr Leu Glu Arg Ala Gly Leu Pro Tyr Gly Val Ala
1 5 10 15
Asp Ala Gly Asp Ile Pro Ala Leu Gly Arg Pro Val Ala Arg Asp Val
20 25 30
Glu Ser Leu Arg Val Glu Arg Leu Ala Ala Pro Ala Ala Ser Ala
35 40 45
Ser Gly Thr Gly Val Ala Leu Thr Pro Pro Ser Ala Ala Ser Gln Gln
50 55 60
Arg Leu Glu Val Ala Asn Arg Ala Glu Ile Ala Ser Leu Val Gln Ala
65 70 75 80
Val Gly Glu Asp Ala Gly Leu Ala Arg Gln Val Val Leu Ala Gly Ala
85 90 95
Ser Thr Leu Leu Ser Ala Gly Leu Met Ser Pro Gln Ala Phe Glu Ile
100 105 110
Glu Leu Ala Lys Ile Thr Gly Glu Val Glu Asn Gln Gln Lys Lys Leu
115 120 125
Lys Leu Thr Glu Ile Glu Gln Ala Arg Lys Gln Asn Leu Gln Lys Met
130 135 140
Glu Asp Asn Gln Gln Lys Ile Arg Glu Ser Glu Glu Ala Ala Lys Glu
145 150 155 160
Ala Gln Lys Ser Gly Leu Ala Ala Lys Ile Phe Gly Trp Ile Ser Ala
165 170 175
Ile Ala Ser Ile Ile Val Gly Ala Ile Met Val Ala Thr Gly Val Gly

	180		185		190												
Ala	Ala	Ala	Gly	Ala	Leu	Met	Ile	Ala	Gly	Gly	Val	Met	Gly	Val	Val		
	195						200					205					
Ser	Gln	Ser	Val	Gln	Gln	Ala	Ala	Ala	Asp	Gly	Leu	Ile	Ser	Lys	Glu		
	210					215					220						
Val	Met	Glu	Lys	Leu	Gly	Pro	Ala	Leu	Met	Gly	Ile	Glu	Ile	Ala	Val		
	225				230					235					240		
Ala	Leu	Leu	Ala	Ala	Val	Val	Ser	Phe	Gly	Gly	Ser	Ala	Val	Gly	Gly		
				245					250					255			
Leu	Ala	Lys	Leu	Gly	Ala	Lys	Ile	Gly	Gly	Lys	Ala	Ala	Glu	Met	Thr		
			260					265					270				
Ala	Ser	Leu	Ala	Ser	Lys	Val	Ala	Asn	Leu	Gly	Gly	Lys	Phe	Gly	Ser		
		275					280						285				
Leu	Ala	Gly	Gln	Ser	Leu	Ser	His	Ser	Leu	Lys	Leu	Gly	Val	Gln	Val		
	290					295					300						
Ser	Asp	Leu	Thr	Leu	Asp	Val	Ala	Asn	Gly	Ala	Ala	Gln	Ala	Thr	His		
	305				310					315					320		
Ser	Gly	Phe	Gln	Ala	Lys	Ala	Ala	Asn	Arg	Gln	Ala	Asp	Val	Gln	Glu		
				325					330					335			
Ser	Arg	Ala	Asp	Leu	Thr	Thr	Leu	Gln	Gly	Val	Ile	Glu	Arg	Leu	Lys		
			340					345					350				
Glu	Glu	Leu	Ser	Arg	Met	Leu	Glu	Ala	Phe	Gln	Glu	Ile	Met	Glu	Arg		
		355					360					365					
Ile	Phe	Ala	Met	Leu	Gln	Ala	Lys	Gly	Glu	Thr	Leu	His	Asn	Leu	Ser		
	370					375					380						
Ser	Arg	Pro	Ala	Ala	Ile												
	385				390												

<210> 44
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 44
 tttttacgtg aagcggggtg

<210> 45
 <211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45
ggcattagcg gatgtctgac tg 22

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 46
caccaggaac cattttctct gg 22

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
cagcgatgac gatattcgac aag 23

<210> 48
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
gaaatcccgc agaaatg 17

<210> 49
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
aaggcataa tataaac 17

<210> 50
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
agagatgtat tagatac 17

<210> 51
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 51
gcaataagag tatcaac 17

<210> 52
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 52
gctaagcttc ggctcaaatt gtttgaaaa c 31

<210> 53
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 53
gctaagctta gagatgtatt agatacc 27

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 54
attggatccg caagcgtcca gaa 23

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 55
tatggatcct cagattaagc gcg 23

<210> 56
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 56
atagaattcg gagggagatg gagtggaag 29

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 57
atagaattcg aagataaagc gattgccgac 30

<210> 58
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 58
gaaggatcca ctccatctcc ctc 23

<210> 59
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

 <400> 59
 gaaggatcca ttgctctat ttcttgc 27

 <210> 60
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 60
 atgggatccg agattcgcca gaatgcgcaa 30

 <210> 61
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 61
 atgggatcca ctggcataaa cggtttccgg 30

 <210> 62
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 62
 attggatcct gacgtaaattc attatca 27

 <210> 63
 <211> 27
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 63
 attggatcct taagcaataa gtgaatc 27

 <210> 64
 <211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 64
aaggaattca acaggcaact ggagg 25

<210> 65
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 65
ctgccctcgc gaaaattaag ataata 26

<210> 66
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 66
cttaattttc gcgaggg 17

<210> 67
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 67
ggacgccctt gggttaata 18

<210> 68
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 68
ggtctgcagg atttttcacg catcgcgctc 29

<210> 69
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 69
ggctctgcaga accattgata tataagctgc 30

<210> 70
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 70
gctgtcgact tgtagtgagt gagcaag 27

<210> 71
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 71
ggatctagat tttagctcct gtcagaaag 29

<210> 72
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 72
ggatctagat ctgaggataa aatatgg 28

<210> 73
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 73

gctgagctct gccgctgacg gaatatg,

27